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OM nucleic - nucleic search, using sw model

Run on: June 21, 2004, 10:27:46 ; Search time 1299 Seconds
(without alignments)
11496.806 Million cell updates/sec

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Perfect score: 3260
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3017426 seqs, 2290544650 residues

Total number of hits satisfying chosen parameters: 6034852

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:
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19: /cgn2_6/ptodata/1/pubnpa/US60_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
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4	3232.6	99.2	4642	15	US-09-842-930A-24
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7	2995.6	91.9	8495	16	US-10-107-782-1
8	2995.6	91.9	8495	16	US-10-028-248A-3
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ALIGNMENTS

RESULT 1

US-10-028-248A-210
Sequence 210, Application US/10028248A
Publication No. US20030235882A1
GENERAL INFORMATION:
APPLICANT: Shimkets, Richard
APPLICANT: Patturajan, Meera
APPLICANT: Vernet, Corine
APPLICANT: Casman, Stacie
APPLICANT: Malyankar, Uriel
APPLICANT: Shenoy, Suresh
APPLICANT: Spytek, Kimberly
APPLICANT: Gangolli, Esha
APPLICANT: Miller, Charles
APPLICANT: Boldog, Ferenc
APPLICANT: Li, Li
APPLICANT: Li, Li
APPLICANT: Taupier Jr, Raymond J
APPLICANT: Kekuda, Ramesh
APPLICANT: Smithson, Glennda
APPLICANT: Zerhusen, Bryan
APPLICANT: Liu, Xiaohong
APPLICANT: Colman, Steven
APPLICANT: Tchernev, Velizar
APPLICANT: Si, Jingsheng
APPLICANT: Edinger, Shlomit
APPLICANT: Stone, David
APPLICANT: Sciore, Paul
APPLICANT: Millet, Isabelle
APPLICANT: Rothenberg, Mark
TITLE OF INVENTION: No. US20030235882A1el Nucleic Acids and Polypeptides and Methods
FILE REFERENCE: 21402-222
CURRENT APPLICATION NUMBER: US/10/028,248A
PRIOR FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/256619
PRIOR FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: 60/262959

Sequence 30654, A
Sequence 610, App
Sequence 1824, Ap
Sequence 12, Appl
Sequence 13, Appl
Sequence 16736, A
Sequence 230, App
Sequence 5045, Ap
Sequence 2410, Ap
Sequence 8459, Ap
Sequence 32777, A
Sequence 1252, Ap
Sequence 58386, A
Sequence 58386, A
Sequence 446, App
Sequence 124, App
Sequence 1, Appli
Sequence 291, App
Sequence 1020, Ap
Sequence 445, App
Sequence 15, Appl
Sequence 880, App
Sequence 18, Appl
Sequence 293, App
Sequence 18, Appl
Sequence 17767, A
Sequence 44, Appl
Sequence 1663, A
Sequence 13589, A
Sequence 488, App

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; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: 60/272408
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/285189
; PRIOR FILING DATE: 2001-04-20
; PRIOR APPLICATION NUMBER: 60/308039
; PRIOR FILING DATE: 2001-07-26
; PRIOR APPLICATION NUMBER: 60/311266
; PRIOR FILING DATE: 2001-08-09
; NUMBER OF SEQ ID NOS: 211
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; SEQ ID NO 210
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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: [317]
; OTHER INFORMATION: Wherein n is A, C, G, or T
US-10-028-248A-210

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; PRIOR FILING DATE: 2001-03-28
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; OTHER INFORMATION: Wherein n may be
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QY 2401 AAACAGGGTGGGAAGCAAGTGTCTCATCTGCGAGCAGACCCACTCGAACCGACGG 2460
Db 2401 AAACAGGGTGGGAAGCAAGTGTCTCATCTGCGAGCAGACCCACTCGAACCGACGG 2460
QY 2461 AGACAGGTTTCTGATGAAGAGCCATTCGCTGAGTGGGACATCTTGTGCTCCAATGGGA 2520
Db 2461 AGACAGGTTTCTGATGAAGAGCCATTCGCTGAGTGGGACATCTTGTGCTCCAATGGGA 2520
QY 2521 TCATTCATGTCTATTTCCAGGCTTTTAAAGACCCCTGCCCCCGTGAACCTTGACCCACA 2580
Db 2521 TCATTCATGTCTATTTCCAGGCTTTTAAAGACCCCTGCCCCCGTGAACCTTGACCCACA 2580
QY 2581 CTGGCTTGGGACAGGGATCTTCTTTGCCATCATCTGCTGAGTGGGGCTGTGCTTGG 2640
Db 2581 CTGGCTTGGGACAGGGATCTTCTTTGCCATCATCTGCTGAGTGGGGCTGTGCTTGG 2640
QY 2641 CTGCTTACTCTTCTTTCGATAAACCGAGAACATCGGCTTCAGACATTTTGAGTCGG 2700
Db 2641 CTGCTTACTCTTCTTTCGATAAACCGAGAACATCGGCTTCAGACATTTTGAGTCGG 2700
QY 2701 AAGAGGACATTAATGTGTCAGCTCTTTGGCAAGCAGAGCTGAGAAATATCTGAAACCCCT 2760
Db 2701 AAGAGGACATTAATGTGTCAGCTCTTTGGCAAGCAGAGCTGAGAAATATCTGAAACCCCT 2760
QY 2761 TGATAGAGACCAACTCAGCTCCCGCAGAACCTTCTACGACCCCTTCAGGACTCTG 2820
Db 2761 TGATAGAGACCAACTCAGCTCCCGCAGAACCTTCTACGACCCCTTCAGGACTCTG 2820
QY 2821 AAGAACGGAGCTTGAGGGCAATGACCCCTTGAGGACACTGTAGGGGCTTGGACGGGAGA 2880
Db 2821 AAGAACGGAGCTTGAGGGCAATGACCCCTTGAGGACACTGTAGGGGCTTGGACGGGAGA 2880
QY 2881 TGCCAGCCATCACTCACTGCACTGGGGCCATCAACTGTGTAATTTCTCAGCACCAGTTGCC 2940
Db 2881 TGCCAGCCATCACTCACTGCACTGGGGCCATCAACTGTGTAATTTCTCAGCACCAGTTGCC 2940
QY 2941 TTTTAGGAACGTAAAGTCTTTTAAAGCACTCAGAAAGCACTACCTCATCTCTGCGGTGATC 3000
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Db 2941 TTTTAGGAACGTAAAGTCTTTTAAAGCACTCAGAAAGCCATACCTCATCTCTGCGGTGATC 3000
QY 3001 TGGGGGTTGTTTCTGTGGGTGAGAGATGTGTGCTGTGCCACCCAGTACAGCTTCTCTCC 3060
Db 3001 TGGGGGTTGTTTCTGTGGGTGAGAGATGTGTGCTGTGCCACCCAGTACAGCTTCTCTCC 3060
QY 3061 TCTGACCCCTTGGGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 3120
Db 3061 TCTGACCCCTTGGGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 3120
QY 3121 TACATGATGCTTAAGTGTGATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 3180
Db 3121 TACATGATGCTTAAGTGTGATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 3180
QY 3181 CCCAGCCCTAGCCAGTGCCTGACACAGGAACCTGTGCACAATAAAGGTTTATGGAAACAG 3240
Db 3181 CCCAGCCCTAGCCAGTGCCTGACACAGGAACCTGTGCACAATAAAGGTTTATGGAAACAG 3240
QY 3241 AAAAAAAGGTTTATGGAAACAG 3260
Db 3241 AAAAAAAGGTTTATGGAAACAG 3260

RESULT 3
US-09-842-930A-24
; Sequence 24, Application US/09842930A
; Publication No. US20020197681A1
; GENERAL INFORMATION:
; APPLICANT: Weigel, Paul
; TITLE OF INVENTION: Identification of Hyaluronan Receptor for Endocytosis
; FILE REFERENCE: 5820.603
; CURRENT APPLICATION NUMBER: US/09/842,930A
; CURRENT FILING DATE: 2001-04-22
; PRIOR APPLICATION NUMBER: 60/245,320
; PRIOR FILING DATE: 2000-11-02
; PRIOR APPLICATION NUMBER: 60/199,538
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 4576
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-842-930A-24

Query Match 99.2%; Score 3232.6; DB 9; Length 4576;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 3238; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 7 AGCAGAGCTTCCCAAGAACCCGAAACCTTCCAGTATTTCTTCCAGTTTGCAGGAGCAT 66
Db 1328 ATCAGAGCTTCCCAAGAACCCGAAACCTTCCAGTATTTCTTCCAGTTTGCAGGAGCAT 1387
QY 67 TCGTGAAGATCTGCTCGGCCCGCCAGCCCTTCCAGTATTTCTTCCAGTTTGCAGGAGCAT 126
Db 1388 TCGTGAAGATCTGCTCGGCCCGCCAGCCCTTCCAGTATTTCTTCCAGTTTGCAGGAGCAT 1447
QY 127 TTGATGAGGAAGCTCGGGTTAAAGACTGGGACAAATAACGTTTAAATGCCCGAGGTTCTTC 186
Db 1448 TTGATGAGGAAGCTCGGGTTAAAGACTGGGACAAATAACGTTTAAATGCCCGAGGTTCTTC 1507
QY 187 GGTACATGTGTGCTGCTGCCACAGCTGCTTCTGGAACAACTGGAATTTGATCTCAATG 246
Db 1508 GGTACATGTGTGCTGCTGCCACAGCTGCTTCTGGAACAACTGGAATTTGATCTCAATG 1567
QY 247 CTACTTCCCTCCAGAGAGCCAAATAGTATCTCTCGTCTCTCAGAGCAGGTTATATAA 306
Db 1568 CTACTTCCCTCCAGAGAGCCAAATAGTATCTCTCGTCTCTCAGAGCAGGTTATATAA 1627
QY 307 ATAAAGGCTTAAGATCATATCCAGTGATATCATCAGTACTAATGCGGATTTGTTATATCA 366
Db 1628 ACATTAAGGCTTAAGATCATATCCAGTGATATCATCAGTACTAATGCGGATTTGTTATATCA 1687
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QY	1027	GGTGCAGCCTGGTGATACAGATCCCAAGGTGCTGCAAGGCTACTTCCGGCGAGACTGTC	1086	QY	2107	AGCTGGGCTATGTGGGAGATGGCTTCTCATGCAGTGGGAACCTGCTGCAGGTCTCGATGT	2166
Db	2414	GGTGACGCTGGTGATACAGATCCCAAGGTGCTGCAAGGCTACTTCCGGCGAGACTGTC	2473	Db	3494	AGGTGGGCTATGTGGGAGATGGCTTCTCATGCAGTGGGAACCTGCTGCAGGTCTCGATGT	3553
QY	1087	AGGCTGCTCCCTGGAGGACAGATGCCCGGTGTATAACCGGGGTGTGCTGCTTGTACAGT	1146	QY	2167	CTTCCCTCCTCACTACAAACTTCTCTGACGGAAGTGTGGCTATTTCACACAGCTCAGCTC	2226
Db	2474	AGGCTGCTCCCTGGAGGACAGATGCCCGGTGTATAACCGGGGTGTGCTGCTTGTACAGT	2533	Db	3554	CTTCCCTCCTCACTACAAACTTCTCTGACGGAAGTGTGGCTATTTCACACAGCTCAGCTC	3613
QY	1147	ACTCGGCCACCGAGAGTGTAAATGCAACACCGGCTTCAATGGGACGGCGTGTAGATGT	1206	QY	2227	GAGCCGCTGATTTCTTAGAACACCTGACCTGTGCTCATTCGCGGGGACCTCTTTGTGTC	2286
Db	2534	ACTCGGCCACCGAGAGTGTAAATGCAACACCGGCTTCAATGGGACGGCGTGTAGATGT	2593	Db	3614	GAGCCGCTGATTTCTTAGAACACCTGACCTGTGCTCATTCGCGGGGACCTCTTTGTGTC	3673
QY	1207	GCTGGCCGGGAGATTTCGGGCTGTATGTCTGCGCTGTGCTGCTCAGACACGACAGT	1266	QY	2287	CACAGAACAGTGGGCTGGGGAGATGAGACCTTGTCTGGCGGGGACATCGACACACAC	2346
Db	2594	GCTGGCCGGGAGATTTCGGGCTGTATGTCTGCGCTGTGCTGCTCAGACACGACAGT	2653	Db	3674	CACAGAACAGTGGGCTGGGGAGATGAGACCTTGTCTGGCGGGGACATCGACACACAC	3733
QY	1267	GGATGATGGCATCAAGGCTCCGGGCTGCGGAGTGTCTGTGAAACGGGGTGGACAGGCCCT	1326	QY	2347	TGCCCCAATGTCAAGCATGTTTTTCTACAATGACCTTGTCAATGGCACACACCTCTCAACGA	2406
Db	2654	GGATGATGGCATCAAGGCTCCGGGCTGCGGAGTGTCTGTGAAACGGGGTGGACAGGCCCT	2713	Db	3734	TGCCCCAATGTCAAGCATGTTTTTCTACAATGACCTTGTCAATGGCACACACCTCTCAACGA	3793
QY	1327	CGTGCACACTCAGGAGTTTTCCCTGCAGTGTACGCTCTCTGCTCTGCTCATGCCA	1386	QY	2407	GGTGGGAAGCAAGCTGCTCATCACTGCCAGCCAGGACCCACTCCAAACGAGAGACCA	2466
Db	2714	CGTGCACACTCAGGAGTTTTCCCTGCAGTGTGTACGCTCTCTGCTCTGCTCATGCCA	2773	Db	3794	GGTGGGAAGCAAGCTGCTCATCACTGCCAGCCAGGACCCACTCCAAACGAGAGACCA	3853
QY	1387	CTGTGAAGAGAACAAACAGTGTGAGTGTAACTCGATTATGAAGGTGACGGAAATCACAT	1446	QY	2467	GGTTTCTTCATGGGAAGAGCATTTCTGCAGTGGGACATCTTTGCTCCCAATGGGATCATTC	2526
Db	2774	CTGTGAAGAGAACAAACAGTGTGAGTGTAACTCGATTATGAAGGTGACGGAAATCACAT	2833	Db	3854	GGTTTCTTCATGGGAAGAGCATTTCTGCAGTGGGACATCTTTGCTCCCAATGGGATCATTC	3913
QY	1447	GCACAGTGTGATTTCTGGAACACAGGACAAACCGGGGCTGTGCAAAAGGTGGCCAGATGCT	1506	QY	2527	ATGTCAATTTCCAGGCTTTTAAAGCACACCCCTGCCCCCGGTGACCTTTGACCCACACCTGGCT	2586
Db	2834	GCACAGTGTGATTTCTGGAACACAGGACAAACCGGGGCTGTGCAAAAGGTGGCCAGATGCT	2893	Db	3914	ATGTCAATTTCCAGGCTTTTAAAGCACACCCCTGCCCCCGGTGACCTTTGACCCACACCTGGCT	3973
QY	1507	CCAGAAAGGCGACGAAGTCTCTGTCAGCTGCCAGAGGAGATCAAGGAGCGGCACA	1566	QY	2587	TGGGACGAGGATCTTTTGGCATCATCTCTGCTGACCTGGGCTGTGGCTGGCTGCTT	2646
Db	2894	CCAGAAAGGCGACGAAGTCTCTGTCAGCTGCCAGAGGAGATCAAGGAGCGGCACA	2953	Db	3974	TGGGACGAGGATCTTTTGGCATCATCTCTGCTGACCTGGGCTGTGGCTGGCTGCTT	4033
QY	1567	GCTGCACAGAGATAGACCCCTGTGTCAGACGGGCTTAAACGAGGGGTGTACGAGCAGCCA	1626	QY	2647	ACTCTTACTTTCCGATATAACCGAGAAACAAATCGGCTTCCAGCATTTTGTAGTGGGAAGG	2706
Db	2954	GCTGCACAGAGATAGACCCCTGTGTCAGACGGGCTTAAACGAGGGGTGTACGAGCAGCCA	3013	Db	4034	ACTCTTACTTTCCGATATAACCGAGAAACAAATCGGCTTCCAGCATTTTGTAGTGGGAAGG	4093
QY	1627	CTGTGAAGATGACAGCCCGGGCAAGCAAGTGTGAGTGTAAAGTCACTATGTCGAG	1686	QY	2707	ACATTAATGTTGAGCTCTTGGCAAGCAGCAGCTGAGAAATATCTCGAACCCCTTGTATG	2766
Db	3014	CTGTGAAGATGACAGCCCGGGCAAGCAAGTGTGAGTGTAAAGTCACTATGTCGAG	3073	Db	4094	ACATTAATGTTGAGCTCTTGGCAAGCAGCAGCTGAGAAATATCTCGAACCCCTTGTATG	4153
QY	1687	ATGGGCTGAATGTGAGCCGAGCAGCTGCCATTGACCGCTCTTACAGGCAATGGC	1746	QY	2767	AGGACACACCTCAGCTCCCGCAGAACCTTCTCAAGACCCCTTCAAGACCCCTCTGAAGAAC	2826
Db	3074	ATGGGCTGAATGTGAGCCGAGCAGCTGCCATTGACCGCTCTTACAGGCAATGGC	3133	Db	4154	AGGACACACCTCAGCTCCCGCAGAACCTTCTCAAGACCCCTTCAAGACCCCTCTGAAGAAC	4213
QY	1747	AGTGCCATGCAGACGCCAAATGTGTCGACCTCCACTTCCAGGATACCACTGTTGGGGTGT	1806	QY	2827	GGCAGCTTGAGGGCAATGACCCCTTGAGGACACTGTGAGGGCTGGACGGGAGATGCCAG	2886
Db	3134	AGTGCCATGCAGACGCCAAATGTGTCGACCTCCACTTCCAGGATACCACTGTTGGGGTGT	3193	Db	4214	GGCAGCTTGAGGGCAATGACCCCTTGAGGACACTGTGAGGGCTGGACGGGAGATGCCAG	4273
QY	1807	TCCATCTAGCTCCCACTGGGCGAGTAAAGTGTGAGTGTAAAGTCACTATGTCGAG	1866	QY	2887	CCATCACTCACTGCGCACCTGGGCCATCAACTGTGAATTTCTCAGCACCAGTTCCTTTAG	2946
Db	3194	TCCATCTAGCTCCCACTGGGCGAGTAAAGTGTGAGTGTAAAGTCACTATGTCGAG	3253	Db	4274	CCATCACTCACTGCGCACCTGGGCCATCAACTGTGAATTTCTCAGCACCAGTTCCTTTAG	4333
QY	1867	GTGCCAACGAAGTGTGACCATGGCAACCTCAACACAGCTCTCTATGCCCCAGAGGCCA	1926	QY	2947	GAACTTAAGTCTTTTAAGCACTCAGAGCCATCACTCATCTCTCTGGCTGATCTGGGG	3006
Db	3254	GTGCCAACGAAGTGTGACCATGGCAACCTCAACACAGCTCTCTATGCCCCAGAGGCCA	3313	Db	4334	GAACTTAAGTCTTTTAAGCACTCAGAGCCATCACTCATCTCTCTGGCTGATCTGGGG	4393
QY	1927	AGTACCACTGTGCTCAGCAGCTGGCTGGAGACCGGGCGGGTTCCTACCCCAAGCCT	1986	QY	3007	TTGTTTCTGTGGGTGAGAGA TGTGTTGTGTGTCGCCACCCAGTACAGCTTCCTCTCTGAC	3066
Db	3314	AGTACCACTGTGCTCAGCAGCTGGCTGGAGACCGGGCGGGTTCCTACCCCAAGCCT	3373	Db	4394	TTGTTTCTGTGGGTGAGAGA TGTGTTGTGTGTCGCCACCCAGTACAGCTTCCTCTCTGAC	4453
QY	1987	TGCGCTCCAGAACTGTGCTCTGTGTGTTGGATAGTGAGCTATGAGCCTAGACCA	2046	QY	3067	CTTTTGGCTCTTCTTCTTGTACTCTTCTCAGCTGGCACTGTCTCCATTCATTCGCTTACATG	3126
Db	3374	TGCGCTCCAGAACTGTGCTCTGTGTGTTGGATAGTGAGCTATGAGCCTAGACCA	3433	Db	4454	CTTTTGGCTCTTCTTCTTGTACTCTTCTCAGCTGGCACTGTCTCCATTCATTCGCTTACATG	4513
QY	2047	ACAAGAGTGAATGTGGAGTGTCTTCTGCTATCGGATGAAGATGTGAAGTGCACCTGCA	2106	QY	3127	ATGGTAACTGTGATCTTTTCTTCTTCTTGTAGATTCTAAGCCTCCNTCTTTGTATCCACG	3186
Db	3434	ACAAGAGTGAATGTGGAGTGTCTTCTGCTATCGGATGAAGATGTGAAGTGCACCTGCA	3493	Db	4514	ATGGTAACTGTGATCTTTTCTTCTTCTTGTAGATTGTAGCCTCCGCTCTTTGTATCCACG	4573
				QY	3187	CCCTAGCCCAAGTGCCTGACACAGGAACCTGTGCACAAATAAAGGTTTATGGAACAGAAAAA	3246

Db 4574 CCCTAGCCAGTCTGCACACAGGAACGTGCACATAAAGGTTTATGGAAACAGAAACAA 4633
Qy 3247 AAAAAAAAA 3254
Db 4634 AGTCAACA 4641

RESULT 5

US-10-028-248A-1
; Sequence 1, Application US/10028248A
; Publication No. US20030235882A1
; GENERAL INFORMATION:
; APPLICANT: Shimkets, Richard
; APPLICANT: Patturajan, Meera
; APPLICANT: Vernet, Corine
; APPLICANT: Casman, Stacie
; APPLICANT: Malyankar, Uriel
; APPLICANT: Shenoy, Suresh
; APPLICANT: Spytek, Kimberly
; APPLICANT: Gangolli, Esha
; APPLICANT: Miller, Charles
; APPLICANT: Boldog, Ferenc
; APPLICANT: Li, Li
; APPLICANT: Taupier Jr, Raymond J
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Smithson, Glennnda
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Liu, Xiaohong
; APPLICANT: Colman, Steven
; APPLICANT: Tchernev, Velizar
; APPLICANT: Si, Jingsheng
; APPLICANT: Edinger, Shlomit
; APPLICANT: Stone, David
; APPLICANT: Sciore, Paul
; APPLICANT: Millet, Isabelle
; APPLICANT: Rothenberg, Mark
; TITLE OF INVENTION: No. US20030235882A1el Nucleic Acids and Polypeptides and Methods
; TITLE OF INVENTION: Thereof
; FILE REFERENCE: 21402-222
; CURRENT APPLICATION NUMBER: US/10/028,248A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/256619
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/262959
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: 60/272408
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/285189
; PRIOR FILING DATE: 2001-04-20
; PRIOR APPLICATION NUMBER: 60/308039
; PRIOR FILING DATE: 2001-07-26
; PRIOR APPLICATION NUMBER: 60/311266
; PRIOR FILING DATE: 2001-08-09
; NUMBER OF SEQ ID NOS: 211
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 8444
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (163)..(168)
; OTHER INFORMATION: wherein n is A, C, G, or T
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1279)..(1284)
; OTHER INFORMATION: wherein n is A, C, G, or T
US-10-028-248A-1

Query Match 92.0%; Score 2999.8; DB 16; Length 8444;
Best Local Similarity 96.1%; Pred. No. 0;
Matches 3128; Conservative 0; Mismatches 18; Indels 108; Gaps 1;

Qy 7 AGCAGGAGCTTCCCAAGAACCCGAAACCTTCCCAAGTATTTCTTCCAGTTGCAGGAGCAATT 66
Db 5279 ATCAGGAGCTTCCCAAGAACCCGAAACCTTCCCAAGTATTTCTTCCAGTTGCAGGAGCAATT 5338
Qy 67 TCCTGAAAGATCTCGTCCGCCAGGCCCTTCACTGTTTTTGGACCTTTATCTGCAGCT 126
Db 5339 TCCTGAAAGATCTCGTCCGCCAGGCCCTTCACTGTTTTTGGACCTTTATCTGCAGCT 5398
Qy 127 TTGATGAGGAAAGCTCGGGTTAAAGACTGGGACAAATACGGTTTAAATGCCAGGTTCTTC 186
Db 5399 TTGATGAGGAAAGCTCGGGTTAAAGACTGGGACAAATACGGTTTAAATGCCAGGTTCTTC 5458
Qy 187 GGTACCATGTGGTCCCTGCCACACAGCTGCTTCTGGAAACCTGAAATGATCAAAATG 246
Db 5459 GGTACCATGTGGTCCCTGCCACACAGCTGCTTCTGGAAACCTGAAATGATCAAAATG 5518
Qy 247 CTACTTCCCTCCAGGAGAGCAATAGTCACTCCGCTCTCAGAGCACGGTGTATATAA 306
Db 5519 CTACTTCCCTCCAGGAGAGCAATAGTCACTCCGCTCTCAGAGCACGGTGTATATAA 5578
Qy 307 ATAATAAGGCTAAGATCATATCCAGTGATATCATCAGTACTAATGGGATTTGTTCAATCA 366
Db 5579 ATAATAAGGCTAAGATCATATCCAGTGATATCATCAGTACTAATGGGATTTGTTCAATCA 5638
Qy 367 TAGACAAATTTGCTATCTCCAAAATTTGCTTTATCATCTCCAAAAGACAACTCTGGAAGAA 426
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Db 5699 TTCTGCAAAATTTACGACTTTGGCAACAAACAAATAGCTAGTCAATCAAAATTTAGCAACTTAA 5758
Qy 487 TACAGGACTCAGGTTTGTGAGTGTATCACCAGTCCCATCCACACCCAGTCACTCTCT 546
Db 5759 TACAGGACTCAGGTTTGTGAGTGTATCACCAGTCCCATCCACACCCAGTCACTCTCT 5818
Qy 547 TCTGCCCAACGACCAAGCCCTCCATGCCCTTACCTGTCTGTAACAAAGACAACTCTCTGTCA 606
Db 5819 TCTGCCCAACGACCAAGCCCTCCATGCCCTTACCTGTCTGTAACAAAGACAACTCTCTGTCA 5878
Qy 607 ACCAAGACAAACAAAGACCAAGCTGGAAGAGTATTTGAAGTTTTCATGTGATACGAGATGCA 666
Db 5879 ACCAAGACAAACAAAGACCAAGCTGGAAGAGTATTTGAAGTTTTCATGTGATACGAGATGCA 5938
Qy 667 AGGTTTATAGTGTGGATCTTCCACATCCACTGCTGGAAGACCTGCAAGGTTGAGAGC 726
Db 5939 AGGTTTATAGTGTGGATCTTCCACATCCACTGCTGGAAGACCTGCAAGGTTGAGAGC 5998
Qy 727 TGAGTGTGAATGTGGAGCTGGCAGGACATCGGTGACCTCTTTCTGAATGGCCAAACCT 786
Db 5999 TGAGTGTGAATGTGGAGCTGGCAGGACATCGGTGACCTCTTTCTGAATGGCCAAACCT 6058
Qy 787 GCAGAAATGTGCAGCGGAGCTCTTTGTTGACCTGGGTGTGGCTACGGCATTTGACTGTC 846
Db 6059 GCAGAAATGTGCAGCGGAGCTCTTTGTTGACCTGGGTGTGGCTACGGCATTTGACTGTC 6118
Qy 847 TGCTGATTTGATCCCAACCTTGGGGGCGCTGTGACACCTTTTACTTTTCGATGCTCGG 906
Db 6119 TGCTGATTTGATCCCAACCTTGGGGGCGCTGTGACACCTTTTACTTTTCGATGCTCGG 6178
Qy 907 GGGAGTGTGGAGCTGTGTCAATCTCCAGCTGCCCAAGTGGAGTAAACCAAGGGTGT 966
Db 6179 GGGAGTGTGGAGCTGTGTCAATCTCCAGCTGCCCAAGTGGAGTAAACCAAGGGTGT 6238
Qy 967 TGAACGAGAAGTGTCTCTACAACTTCCCTTCAAGAGGAACCTGGAAGGCTCCCGGAGC 1026
Db 6239 TGAACGAGAAGTGTCTCTACAACTTCCCTTCAAGAGGAACCTGGAAGGCTCCCGGAGC 6298
Qy 1027 GGTGACGCTGTGTATACAGATCCCAAGGCTGTGCAAGGGCTACTTTCGGGCGAGACTGTC 1086
Db 6299 GGTGACGCTGTGTATACAGATCCCAAGGCTGTGCAAGGGCTACTTTCGGGCGAGACTGTC 6358

QY	1087	AGGCTGCTCCCTGAGGACAGATGCCCCGCTGTAATAACCGGGTGTCTGCTTGTATCAGT	1146		7359	-----GGAGTGTGGCTATTCCAAAGCTCAGCTC	7390	
Db	6359	AGGCTGCTCCCTGAGGACAGATGCCCCGCTGTAATAACCGGGTGTCTGCTTGTATCAGT	6418					
QY	1147	ACTCGGCGACCGAGAGTGTAAATGCAACAACCGGCTTCAATGGGACGGCGTGTGAGATGT	1206					
Db	6419	ACTCGGCGACCGAGAGTGTAAATGCAACAACCGGCTTCAATGGGACGGCGTGTGAGATGT	6478					
QY	1207	GCTGGCGGGGAGATTGGGCTTGATTTGCTGCTGCTGCTGCTGCTCAGACCAAGGACGT	1266					
Db	6479	GCTGGCGGGGAGATTGGGCTTGATTTGCTGCTGCTGCTGCTCAGACCAAGGACGT	6538					
QY	1267	GCATGATGGCATCAGCGGCTCCGGGCACTGCTCTGTGAACCGGGTGAACAGGCGCCCT	1326					
Db	6539	GCATGATGGCATCAGCGGCTCCGGGCACTGCTCTGTGAACCGGGTGAACAGGCGCCCT	6598					
QY	1327	CGTGTGACACTCAGGACGATTTGCCCTGCACTGTGTAGCGCTCCTTGTTCGTCTCATGCCA	1386					
Db	6599	CGTGTGACACTCAGGACGATTTGCCCTGCACTGTGTAGCGCTCCTTGTTCGTCTCATGCCA	6658					
QY	1387	CCTGTAAGGAGAACACAGCTGTGAGTGTAACTGGATTATGAAGTGTGACGGATCACAT	1446					
Db	6659	CCTGTAAGGAGAACACAGCTGTGAGTGTAACTGGATTATGAAGTGTGACGGATCACAT	6718					
QY	1447	GCACAGTTGTGGATTTCTGCAACAGACACAAACCGGGGCTGTGCAAAAGGTGGCCAGATGCT	1506					
Db	6719	GCACAGTTGTGGATTTCTGCAACAGACACAAACCGGGGCTGTGCAAAAGGTGGCCAGATGCT	6778					
QY	1507	CCGAGAAGGGCAGAAAGTCTCTGACAGTGCAGAGGGAATCAAAAGGGGACGGGCA	1566					
Db	6779	CCGAGAAGGGCAGAAAGTCTCTGACAGTGCAGAGGGAATCAAAAGGGGACGGGCA	6838					
QY	1567	GCTGACAGAGATAGACCCCTGTGACAGCGGCTTAAACGAGGGTGTACAGGACGCGCA	1626					
Db	6839	GCTGACAGAGATAGACCCCTGTGACAGCGGCTTAAACGAGGGTGTACAGGACGCGCA	6898					
QY	1627	CCTGTAAGATGACAGCCCGGCAAGCAAGTGTGAGTGTAAAGTCACTATGTCGGAG	1686					
Db	6899	CCTGTAAGATGACAGCCCGGCAAGCAAGTGTGAGTGTAAAGTCACTATGTCGGAG	6958					
QY	1687	ATGGGCTGAATGTGACCGGAGCAGCTGCCATTTGACCGCTTTACAGGACAAATGGGC	1746					
Db	6959	ATGGGCTGAATGTGACCGGAGCAGCTGCCATTTGACCGCTTTACAGGACAAATGGGC	7018					
QY	1747	AGTGCCATGACAGCGCAAAATGTGCGACTCCACTTCCAGGATACCACTGTTGGGGTGT	1806					
Db	7019	AGTGCCATGACAGCGCAAAATGTGCGACTCCACTTCCAGGATACCACTGTTGGGGTGT	7078					
QY	1807	TCCATCTACGCTCCCACTGGGCGAGTATAAGCTGACCTTTGACAAAGCCAGAGAGGCT	1866					
Db	7079	TCCATCTACGCTCCCACTGGGCGAGTATAAGCTGACCTTTGACAAAGCCAGAGAGGCT	7138					
QY	1867	GTGCCAACGAAGTGGACATGGCAACTACACAGCTCTCTATGCCCAGAGGCCA	1926					
Db	7139	GTGCCAACGAAGTGGACATGGCAACTACACAGCTCTCTATGCCCAGAGGCCA	7198					
QY	1927	AGTACCACCTGTGCTCAGCAGGCTGGCTGGAGACCGGGCGGTGTGCTACCCCAAGGCT	1986					
Db	7199	AGTACCACCTGTGCTCAGCAGGCTGGCTGGAGACCGGGCGGTGTGCTACCCCAAGGCT	7258					
QY	1987	TGCGCTCCAGAACTGTGCTCTGGCTCTGGTGTGGATAGTGAATGACCTAGACCCA	2046					
Db	7259	TGCGCTCCAGAACTGTGCTCTGGTGTGGTGTGGATAGTGAATGACCTAGACCCA	7318					
QY	2047	ACAAGAGTGAATGTGGGATGCTCTGCTATCGATGGAATGGAATGGAATGGAATGGA	2106					
Db	7319	ACAAGAGTGAATGTGGGATGCTCTGCTATCGATGGAATGGAATGGAATGGAATGGA	7358					
QY	2107	AGGTGGGCTATGTGGGAGATGGCTTCTCATGAGTGGGAACTGCTGAGGTCTCTGATGT	2166					
Db	7359	-----	7358					
QY	2167	CCTTCCCTCACTCACAACCTTCCTGACGGAGTGTGGCCTATTCCAAACAGCTCAGCTC	2226					

QY	247	CTACTTCCCTCCAAGGAGGCCAATAGTATCATCTCCGCTCTCTCAGAGCACGGTGTATATAA	306
Db	5519	CTACTTCCCTCCAAGGAGGCCAATAGTATCATCTCCGCTCTCTCAGAGCACGGTGTATATAA	5578
QY	307	ATAATAAGGCTAAGATCATATCCAGTGAATCATCATAGTACTAATGGATTGTTCAATCA	366
Db	5579	ATAATAAGGCTAAGATCATATCCAGTGAATCATCATAGTACTAATGGATTGTTCAATCA	5638
QY	367	TAGACAAATGCTATCTCCAAAATTTGGTTATCACTCCCAAAGAACAATCTGGGAAGAA	426
Db	5639	TAGACAAATGCTATCTCCAAAATTTGGTTATCACTCCCAAAGAACAATCTGGGAAGAA	5698
QY	427	TTCTGCAAAATCTTACGACTTTGGCAACAAACAAATGCTACATCAAAATTTAGCAACTTAA	486
Db	5699	TTCTGCAAAATCTTACGACTTTGGCAACAAACAAATGCTACATCAAAATTTAGCAACTTAA	5758
QY	487	TACAGACTCAGGTTTGTGAGTGTATCAACCGATCCCATCCACACCCCAAGTCACTCTCT	546
Db	5759	TACAGACTCAGGTTTGTGAGTGTATCAACCGATCCCATCCACACCCCAAGTCACTCTCT	5818
QY	547	TCTGGCCCAACGACCAAGCCCTCCATGCCCTACCTGCTGAACAAAGGACTTCTCTTTCA	606
Db	5819	TCTGGCCCAACGACCAAGCCCTCCATGCCCTACCTGCTGAACAAAGGACTTCTCTTTCA	5878
QY	607	ACCAAGACAAAGGACAAAGCTGAAGAGTATTTGAAGTTTCAATGTATACGAGATGCCA	666
Db	5879	ACCAAGACAAAGGACAAAGCTGAAGAGTATTTGAAGTTTCAATGTATACGAGATGCCA	5938
QY	667	AGGTTTATGCTGGATCTTCCOACATCCATGCTGGAAGACCCCTGCAAGGTTTCAGAGC	726
Db	5939	AGGTTTATGCTGGATCTTCCOACATCCATGCTGGAAGACCCCTGCAAGGTTTCAGAGC	5998
QY	727	TGAGTGTGAATGTGAGCTGGCAGGACATCGGTGACCTTTCTGGAATGGCCAAACCT	786
Db	5999	TGAGTGTGAATGTGAGCTGGCAGGACATCGGTGACCTTTCTGGAATGGCCAAACCT	6058
QY	787	GCAGAAATGTGACGGGAGCTCTTGTGTAAGCTGGGTGGCTACGGCATTTGACTGTC	846
Db	6059	GCAGAAATGTGACGGGAGCTCTTGTGTAAGCTGGGTGGCTACGGCATTTGACTGTC	6118
QY	847	TGCTGATGATCCCACTCGGGGGCCGCTGTGACACCTTTACTTTGATGCTCGG	906
Db	6119	TGCTGATGATCCCACTCGGGGGCCGCTGTGACACCTTTACTTTGATGCTCGG	6178
QY	907	GGGAGTGTGGAGCTGTGTAATCTCCAGCTGCCAGGTGGAGTAACCAAGGGTG	966
Db	6179	GGGAGTGTGGAGCTGTGTAATCTCCAGCTGCCAGGTGGAGTAACCAAGGGTG	6238
QY	967	TGAAGCAGAAGTGTCTCTACAACCTGCCCTTCAAGAGGAACCTGGAAGGCTGCCGGAGC	1026
Db	6239	TGAAGCAGAAGTGTCTCTACAACCTGCCCTTCAAGAGGAACCTGGAAGGCTGCCGGAGC	6298
QY	1027	GGTGACGCTGTGTATACAGATCCCGAGTGTGCNAAGGGCTACTTCGGGCGAGACTGTC	1086
Db	6299	GGTGACGCTGTGTATACAGATCCCGAGTGTGCNAAGGGCTACTTCGGGCGAGACTGTC	6358
QY	1087	AGGCTTCCCTGGAGGACAGATGCCCGTGTAAATAACCGGGGTGCTCCCTTGATCAGT	1146
Db	6359	AGGCTTCCCTGGAGGACAGATGCCCGTGTAAATAACCGGGGTGCTCCCTTGATCAGT	6418
QY	1147	ACTCGGCCACCGGAGAGTGTAAATGCAACACCGGCTTCAATGGGACGGCGTGTGAGATGT	1206
Db	6419	ACTCGGCCACCGGAGAGTGTAAATGCAACACCGGCTTCAATGGGACGGCGTGTGAGATGT	6478
QY	1207	GCTGGCCGGGAGATTCGGGCTGATTTGCTGCCCTGGCTGTGCTGACACCGAGACTGTC	1266
Db	6479	GCTGGCCGGGAGATTCGGGCTGATTTGCTGCCCTGGCTGTGCTGACACCGAGACTGTC	6538
QY	1267	GGGATGATGGCATCAGGGCTCGGGCAGTGGCTCTGTGAACGGGGTGGACAGGCCCT	1326
Db	6539	GGGATGATGGCATCAGGGCTCGGGCAGTGGCTCTGTGAACGGGGTGGACAGGCCCT	6598
QY	1327	CGTGTGACACTCAGGCAGTCTTTGCCCTCGAGTGTGTACGCTCTTGTCTGCTCATGCCA	1386
Db	6599	CGTGTGACACTCAGGCAGTCTTTGCCCTCGAGTGTGTACGCTCTTGTCTGCTCATGCCA	6658
QY	1387	CCTGTAAAGGAGAACACAGCTGTAGTGTAACTCGATTATGAAGGTGACGGAAATCACAT	1446
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QY	1447	GACAGTTGTGATTTCTGAAAACAGGACAAACGGGGGCTGTGCAAAAGGTGGCCAGATGCT	1506
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QY	1507	CCAGAAAGGCGACGAAGGTCTCTGACAGCTGCCAGAGGAGATACAAAGGGGACGGGACCA	1566
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QY	1567	GCTGCACAGAGATAGACCCCTGTGACAGACGGCCCTTAACGGAGGGTGTACAGACACGCCA	1626
Db	6839	GCTGCACAGAGATAGACCCCTGTGACAGACGGCCCTTAACGGAGGGTGTACAGACACGCCA	6898
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QY	1687	ATGGGCTGAATGTGAGCGGGACAGCTGCCCATTTGACCGCTTACAGGACCAATGGGC	1746
Db	6959	ATGGGCTGAATGTGAGCGGGACAGCTGCCCATTTGACCGCTTACAGGACCAATGGGC	7018
QY	1747	AGTGCCATGCAGACGCCAAATGTGACCTCCACTTCCAGGATACCACTGTTGGGGTGT	1806
Db	7019	AGTGCCATGCAGACGCCAAATGTGACCTCCACTTCCAGGATACCACTGTTGGGGTGT	7078
QY	1807	TCCATCTAGCTCCCACTGGGCCAGTATAAGTGTGAGTGTGACAAAGCCAGAGGCT	1866
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Db	7199	AGTACCACTGTGCTCAGCAGCTGGCTGGAGACCGGGGGGTGCTTACCCACACAGCT	7258
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QY	2047	ACAAGAGTGAAATGTGGGATGTCTTCTGCTATCGGATGAAAGATGTGAACCTGACCTGCA	2106
Db	7319	ACAAGAGTGAAATGTGGGATGTCTTCTGCTATCGGATGAA	7358
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QY	2227	GAGGCGGTGCAATTTCTAGAACACCTGACTGACTTCCATCCGCGGACCCCTCTTTGTGC	2286
Db	7391	GAGGCGGTGCAATTTCTAGAACACCTGACTGACTTCCATCCGCGGACCCCTCTTTGTGC	7450
QY	2287	CACAGAACAGTGGGTGGGGAGAAATGAGACTTGTCTGGGGGGGACATCGAGCACACC	2346
Db	7451	CACAGAACAGTGGGTGGGGAGAAATGAGACTTGTCTGGGGGGGACATCGAGCACACC	7510
QY	2347	TGCGCAATGTGAGCATGTTTTTCTCAATGACTTGTCAATGGCACCCCTGCAAAACCA	2406
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QY	2407	GGGTGGGAAGCAAGCTGCTCATCTGCGCAGCAGGACCCCACTCCAAACCGAGAGACCA	2466

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QY 2527 ATGTCAATTTCCAGGCGCTTTAAAGACACCCCTTGCCCGGTGACCTTGAACCCACATGGCT 2586
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RESULT 7

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; Sequence 3, Application US/10028248A
; Publication No. US20030235882A1
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; APPLICANT: Shimketa, Richard
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; APPLICANT: Spytek, Kimberly
; APPLICANT: Gangolli, Esha
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; APPLICANT: Miller, Charles
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; APPLICANT: Li, Li
; APPLICANT: Taupier Jr, Raymond J
; APPLICANT: Kekuda, Ramesh
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; APPLICANT: Liu, Xiaohong
; APPLICANT: Colman, Steven
; APPLICANT: Tchernev, Velizar
; APPLICANT: Si, Jingsheng
; APPLICANT: Edinger, Shlomit
; APPLICANT: Stone, David
; APPLICANT: Sciore, Paul
; APPLICANT: Millet, Isabelle
; APPLICANT: Rothenberg, Mark
; TITLE OF INVENTION: No. US20030235882A1el Nucleic Acids and Polypeptides and Methods
; TITLE OF INVENTION: Thereof
; FILE REFERENCE: 21402-222
; CURRENT APPLICATION NUMBER: US/10/028,248A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/256619
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/262959
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: 60/272408
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/285189
; PRIOR FILING DATE: 2001-04-20
; PRIOR APPLICATION NUMBER: 60/308039
; PRIOR FILING DATE: 2001-07-26
; PRIOR APPLICATION NUMBER: 60/311266
; PRIOR FILING DATE: 2001-08-09
; NUMBER OF SEQ ID NOS: 211
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 8495
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc-feature
; LOCATION: (131)..(1316)
; OTHER INFORMATION: Wherein n is A, C, G, or T
US-10-028-248A-3
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Query Match 91.9%; Score 2995.6; DB 16; Length 8495;

Best Local Similarity 96.1%; Pred No. 0;

Matches 3137; Conservative 0; Mismatches 10; Indels 116; Gaps 2;

QY 7 AGCAGGAGCTTCCCAAGAACCCGAAACTTCCAGTATTTCTTCCAGTTGCGAGGACATT 66

Db 5311 ATCAGGAGCTTCCCAAGAACCCGAAACTTCCAGTATTTCTTCCAGTTGCGAGGACATT 5370

QY 67 TCGTGAAGATCTGCTCGGCCCGAGCCCTTCACTGTTTTCACCTTTATTCGAGGCT 126

Db 5371 TCGTGAAGATCTGCTCGGCCCGAGCCCTTCACTGTTTTCACCTTTATTCGAGGCT 5430

QY 127 TTGATGAGCAAGCTCGGGTTAAAGACTGGGACAAATACGGTTTAAATGCCAGGTTCTTC 186

Db 5431 TTGATGAGCAAGCTCGGGTTAAAGACTGGGACAAATACGGTTTAAATGCCAGGTTCTTC 5490

QY 187 GGTACCATGTGGTGGCTGCCGCCAGCAGCTGCTTCTGGAAAAACCTGAAATTTGATCTCAAAATG 246

Db 5491 GGTACCATGTGGTGGCTGCCGCCAGCAGCTGCTTCTGGAAAAACCTGAAATTTGATCTCAAAATG 5550

QY 247 CTACTTCCCTCCAGGAGAGCCAAATAGTCATCTCGTCTCTCAGNACCGGTGTATATAA 306

Db 5551 CTACTTCCCTCCAGGAGAGCCAAATAGTCATCTCGTCTCTCAGNACCGGTGTATATAA 5610

QY 307 ATAATAAGGCTAAAGATCATATCCAGTGATATCATCAGTACTAATGGGATTTGTTTATATCA 366

Db 5611 ACAATAAGGCTAAAGATCATATCCAGTGATATCATCAGTACTAATGGGATTTGTTTATATCA 5670

QY	367	TAGACAAATTGCTATCTCCAAAAATTTGCTTATCACTCCAAAGACAACTCTGGAAGAA	426	Db	6751	GAATCACATGCAGTTGTGGATTTCTGCAAAACAGGACAACTGTGCAAAAGGTGG	6810
Db	5671	TAGACAAATTGCTATCTCCAAAAATTTGCTTATCACTCCAAAGACAACTCTGGAAGAA	5730	QY	1498	CCAGATGCTCCCAAGAGGGCAAGAGGTCTCTGAGAGTGCACAGAGGGATACAAAGGGG	1557
QY	427	TTCTGCAAAATCTTACGACTTTGGCAACAAACAAATGGCTACATCAAAATTTAGCAACTTAA	486	Db	6811	CCAGATGCTCCCAAGAGGGCAAGAGGTCTCTCTGCAAGTCCCAAGAGGGATACAAAGGGG	6870
Db	5731	TTCTGCAAAATCTTACGACTTTGGCAACAAACAAATGGCTACATCAAAATTTAGCAACTTAA	5790	QY	1558	ACGGGCACAGCTGCACAGAGATAGACCCCTGTGACAGCGGCTTTAAACGGAGGTGTCAAG	1617
QY	487	TACAGACTCAGTTTCTGAGTGTATCATCCCGATCCCATCCACCCAGTCACTCTCT	546	Db	6871	ACGGGCACAGCTGCACAGAGATAGACCCCTGTGACAGCGGCTTTAAACGGAGGTGTCAAG	6930
Db	5791	TACAGACTCAGTTTCTGAGTGTATCATCCCGATCCCATCCACCCAGTCACTCTCT	5850	QY	1618	AGCACGCCACCTGTAAAGATGACAGGCCCCGGGCAAGCACAAAGTGTAGTGTAAAGTCACT	1677
QY	547	TCCTGGCCCAACGACCAA-----GCCCTCCATGCCCTTACCTGTGTAACACAGGACT	597	Db	6931	AGCACGCCACCTGTAAAGATGACAGGCCCCGGGCAAGCACAAAGTGTAGTGTAAAGTCACT	6990
Db	5851	TCCTGGCCCAACGACCAA-----GCCCTCCATGCCCTTACCTGTGTAACACAGGACT	5910	QY	1678	ATGTCCGAGATGGGCTGAACTGTGAGCCGAGCAGCTGCCATTGACCCGTGTACAGG	1737
QY	598	TCTGTTCACCAAGACAACAAGACAAGCTGAAGGAGTATTTGAAGTTTCATGTGATAC	657	Db	6991	ATGTCCGAGATGGGCTGAACTGTGAGCCGAGCAGCTGCCATTGACCCGTGTACAGG	7050
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QY	658	GAGATGCCAAGTTTGTAGTGTGGATCTTCCACATCCACTGCTCGAAGACCCCTCAAG	717	Db	7051	ACAAATGGGCAAGTGCAGAGCAGCGCAAAATGTGTCCACCTCCACTTCCAGGATACCACTG	7110
Db	5971	GAGATGCCAAGTTTGTAGTGTGGATCTTCCACATCCACTGCTCGAAGACCCCTCAAG	6030	QY	1798	TTGGGCTGTTCATCTACCTCCCACTCGGCGCAGTATTAAGCTGACCTTTGACAAAGCCA	1857
QY	718	GTTTCAGAGCTGAGTGTGAATGTGGAGCTGGCAGGAGACATCGGTGACCTCTTTCTGAATG	777	Db	7111	TTGGGCTGTTCATCTACCTCCCACTCGGCGCAGTATTAAGCTGACCTTTGACAAAGCCA	7170
Db	6031	GTTTCAGAGCTGAGTGTGAATGTGGAGCTGGCAGGAGACATCGGTGACCTCTTTCTGAATG	6090	QY	1858	GAGAGCCCTGTGCGCAACGAGCTGCACCATGGCAACCTTACACAGCTCTCCATATGCC	1917
QY	778	GCCAAACCTGAGAAATGTGAGCGGAGCTCTTTGTTGACCTTGGGTGTGGCCTACGGCA	837	Db	7171	GAGAGCCCTGTGCGCAACGAGCTGCACCATGGCAACCTTACACAGCTCTCCATATGCC	7230
Db	6091	GCCAAACCTGAGAAATGTGAGCGGAGCTCTTTGTTGACCTTGGGTGTGGCCTACGGCA	6150	QY	1918	AGAAGCCCAAGTACCACTGTGCTCAGCAGGCTGGCTGGAGACCCGGCGGTGGCTACC	1977
QY	838	TTGACTGTCTGCTGATTTGATCCACCTCGGGGGCGCTGTGACACCTTTACTACTTTG	897	Db	7231	AGNAGCCCAAGTACCACTGTGCTCAGCAGGCTGGCTGGAGACCCGGCGGTGGCTACC	7290
Db	6151	TTGACTGTCTGCTGATTTGATCCACCTCGGGGGCGCTGTGACACCTTTACTACTTTG	6210	QY	1978	CCACAGCTTCGCTCCCAAGAACTGTGGCTCTGGTGTGGTGGATAGTGGACTATGGAC	2037
QY	898	ATGCTTCGGGGAGTGTGGAGTGTGTCAATACTCCAGCTGCCAAAGTGGAGTAAAC	957	Db	7291	CCACAGCTTCGCTCCCAAGAACTGTGGCTCTGGTGTGGTGGATAGTGGACTATGGAC	7350
Db	6211	ATGCTTCGGGGAGTGTGGAGTGTGTCAATACTCCAGCTGCCAAAGTGGAGTAAAC	6270	QY	2038	CTAGACCCCAAGAGTGAATGTGGATGTCTTCTGCTATCGGATGGAAGATGTGNACT	2097
QY	958	CAAGGGTGTGAAGCAAGTGTCTCTCAACCTGCGCTTCAAGAGGAACCTGGAAGGCT	1017	Db	7351	CTAGACCCCAAGAGTGAATGTGGATGTCTTCTGCTATCGGATGGAAGATGTGNACT	7400
Db	6271	CAAGGGTGTGAAGCAAGTGTCTCTCAACCTGCGCTTCAAGAGGAACCTGGAAGGCT	6330	QY	2098	GCACCTGCAAGGTGGGCTATGTGGGAGATGGCTTCTCATGCACTGGGAACTCTGTCAGG	2157
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QY	1258	ACGGAAGTGCATGATGAGATCAACGGGCTTCGGGAGTGCCTCTCTGTAAACCGGGTGA	1317	Db	7544	AGCACCACTCTGCGCAATGTGAGATGTTTTTTCTAAGTACCTTTGTCAATGGGACCAACC	7603
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RESULT 8

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; Sequence 3, Application US/10107782

; Publication No. US20040018970A1

; GENERAL INFORMATION:

; APPLICANT: Boldog, Ferenc,

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; APPLICANT: Colman, Steve,

; APPLICANT: Edinger, Shlomit,

; APPLICANT: Gangolli, Esha,

; APPLICANT: Kekuda, Ramesh,

; APPLICANT: Li, Li,

; APPLICANT: Liu, Xiaohong,

; APPLICANT: Malyankar, Uriel,

; APPLICANT: Miller, Charles,

; APPLICANT: Millet, Isabelle,

; APPLICANT: Patturajan, Meera,

; APPLICANT: Rothenberg, Mark,

; APPLICANT: Sciore, Paul,

; APPLICANT: Shenoy, Suresh,

; APPLICANT: Shimkets, Richard,

; APPLICANT: Si, Jingsheng,

; APPLICANT: Smithson, Glenda,
; APPLICANT: Spytek, Kimberly,
; APPLICANT: Stone, David,
; APPLICANT: Taupier, Raymond, Jr.,
; APPLICANT: Tchernev, Velizar,
; APPLICANT: Vernet, Corine,
; APPLICANT: Zernusen, Brian
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES AND METHODS OF USE THEREOF
; FILE REFERENCE: 21402-222CIP
; CURRENT APPLICATION NUMBER: US/10/107,782
; PRIOR FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: 10/028,248
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/256,619
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/262,959
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: 60/272,408
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/285,189
; PRIOR FILING DATE: 2001-04-20
; PRIOR APPLICATION NUMBER: 60/308,039
; PRIOR FILING DATE: 2001-07-26
; PRIOR APPLICATION NUMBER: 60/311,266
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 60/279,344
; PRIOR FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 3
; LENGTH: 8495
; TYPE: DNA
; ORGANISM: Homo sapiens
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; OTHER INFORMATION: Wherein Xaa may be any naturally occurring amino acid
; US-10-107-782-3

Query Match

91.9%; Score 2995.6; DB 16; Length 8495;

Best Local Similarity 96.1%; Fred.No. 0;

Matches 3137; Conservative 0; Mismatches 10; Indels 116; Gaps 2;

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QY	67	TGCTGAAAGATCTGGTCGGCCAGGCCCCCTTCACTGTTTTGTGACACCTTTATCTGCAGCCT	126
Db	5371	TGCTGAAAGATCTGGTCGGCCAGGCCCCCTTCACTGTTTTGTGACACCTTTATCTGCAGCCT	5430
QY	127	TTGATGAGGAAGCTCGGGTTAAAGACTGGGACAAATACGGTTTAAATGCCCCAGGTTCTTC	186
Db	5431	TTGATGAGGAAGCTCGGGTTAAAGACTGGGACAAATACGGTTTAAATGCCCCAGGTTCTTC	5490
QY	187	GGTACCATTGTCGCTGCCACCAAGCTGCTTCTGGAACCTGGAATATGATCTCAAAATG	246
Db	5491	GGTACCATTGTCGCTGCCACCAAGCTGCTTCTGGAACCTGGAATATGATCTCAAAATG	5550
QY	247	CTACTTCCCTCCAAAGGAGACCAATAGTCACTCCGTCCTCAGAGCACGGTGTATATAA	306
Db	5551	CTACTTCCCTCCAAAGGAGACCAATAGTCACTCCGTCCTCAGAGCACGGTGTATATAA	5610
QY	307	ATAAATAGGCTAAGATCATATCCAGTGATATCATCATGACTAATGGGATTTGTTCAATCA	366
Db	5611	ACAATAAGGCTAAGATCATATCCAGTGATATCATCATGACTAATGGGATTTGTTCAATCA	5670
QY	367	TAGACAAATTTGCTATCTCCCAAAATTTGCTTATCACTCCCAAGACAACTCTGGAAGAA	426
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QY	427	TTCTGCAAAATCTTACGACTTTTGGCAACAAACAAATGGCTACATCAAAATTTAGCAACTTA	486
Db	5731	TTCTGCAAAATCTTACGACTTTTGGCAACAAACAAATGGCTACATCAAAATTTAGCAACTTA	5790
QY	487	TACAGACTCAGTTTGTGAGTGTATACCCGATCCGATCCACACCCGAGTCACTCTCT	546
Db	5791	TACAGACTCAGTTTGTGAGTGTATACCCGATCCGATCCACACCCGAGTCACTCTCT	5850
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Db	5851	TCGTGCCCCACGACCAAAGCCCTCCATGCCCTCCATGCCCTPACCTGCTGAAACAACAGACT	5910
QY	598	TCCTGTTCAACCAAGACAACAAGGACAGCTGAGGAGTATTTGAAGTTTCATGTGATAC	657
Db	5911	TCCTGTTCAACCAAGACAACAAGGACAGCTGAGGAGTATTTGAAGTTTCATGTGATAC	5970
QY	658	GAGATGCCAAGTTTGTAGTGTGGATCTTCCACATCCACTGCTGGAAGACCCCTGCAAG	717
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QY	718	GTTTCAGAGCTGAGTGTGAATGTGGAGCTGGCAGGGACATCGGTGACCTCTTTCTGAATG	777
Db	6031	GTTTCAGAGCTGAGTGTGAATGTGGAGCTGGCAGGGACATCGGTGACCTCTTTCTGAATG	6090
QY	778	GCCAAACCTGCAGAAATGTGACGGGAGCTTTGTTTGTACCTGGGTGTGGCCTACGGCA	837
Db	6091	GCCAAACCTGCAGAAATGTGACGGGAGCTTTGTTTGTACCTGGGTGTGGCCTACGGCA	6150
QY	838	TTGACTGTCTGCTGATGTATCCACCTGGGGGGCGCTGTGACACCTTTACTACTTTG	897
Db	6151	TTGACTGTCTGCTGATGTATCCACCTGGGGGGCGCTGTGACACCTTTACTACTTTG	6210
QY	898	ATGCCTCGGGGAGTGTGGAGTGTGTCAATACTCCAGCTGCCAAGGTGGAGTAAAC	957
Db	6211	ATGCCTCGGGGAGTGTGGAGTGTGTCAATACTCCAGCTGCCAAGGTGGAGTAAAC	6270
QY	958	CAAGGGTGTGAAGCAAGTGTCTTCAAACTGCCCTTCAAGAGAACTCTGAAGGCT	1017
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QY	1018	GCCGGGAGCGTGCAGCTGTGTATACAGATCCCGAGGTGCTGCAAGGGTACTTCGGG	1077
Db	6331	GCCGGGAGCGTGCAGCTGTGTATACAGATCCCGAGGTGCTGCAAGGGTACTTCGGG	6390
QY	1078	GAGATGTCTCAGGCTCGCCCTGGAGGACCCAGATGCCCGTGTATAAACCGGGGTGTCTGCC	1137
Db	6391	GAGATGTCTCAGGCTCGCCCTGGAGGACCCAGATGCCCGTGTATAAACCGGGGTGTCTGCC	6450
QY	1138	TTGATCAGTACTCGGCCACCGGAGAGTGAATGAACAACCGGCTTCAATGGGACCGCGT	1197
Db	6451	TTGATCAGTACTCGGCCACCGGAGAGTGAATGAACAACCGGCTTCAATGGGACCGCGT	6510
QY	1198	GTGAGATGTCTGGCCCGGGAGATTCGGGCTGTATGTCTGCCCTGTGCTGCTCTAGACC	1257
Db	6511	GTGAGATGTCTGGCCCGGGAGATTCGGGCTGTATGTCTGCCCTGTGCTGCTCTAGACC	6570
QY	1258	ACGACAGTGCATGATGTCATCACGGGCTCCGGGCACTGCCCTCTGTGAAAACGGGGTGA	1317
Db	6571	ACGACAGTGCATGATGTCATCACGGGCTCCGGGCACTGCCCTCTGTGAAAACGGGGTGA	6630
QY	1318	CAGGCCCTCGTGTGACACTCAGGCAAGTTTGTCTCAGTGTGTACGCTCTCTTGTCTTG	1377
Db	6631	CAGGCCCTCGTGTGACACTCAGGCAAGTTTGTCTCAGTGTGTACGCTCTCTTGTCTTG	6690
QY	1378	CTCATGCCACCTGTAAAGGAGAAACAACCTGTGAGTGTAACTGGATTATGAAGGTGACG	1437
Db	6691	CTCATGCCACCTGTAAAGGAGAAACAACCTGTGAGTGTAACTGGATTATGAAGGTGACG	6750
QY	1438	GAATCATATGCAAGTGTGTGATTTCTGCAAAACAGACAAACGGGGCTGTGCAAAAGTGG	1497
Db	6751	GAATCATATGCAAGTGTGTGATTTCTGCAAAACAGACAAACGGGGCTGTGCAAAAGTGG	6810
QY	1498	CCAGATGTCTCCAGAAAGGGCAAGAGTCTCTGCAAGCTGCAAGAGGATACAAAGGGG	1557
Db	6811	CCAGATGTCTCCAGAAAGGGCAAGAGTCTCTGCAAGCTGCAAGAGGATACAAAGGGG	6870
QY	1558	ACGGGCACAGCTGCACAGAGATAGACCCCTGTGCAGACGCGCTTAAACGGAGGGTGTCAAG	1617
Db	6871	ACGGGCACAGCTGCACAGAGATAGACCCCTGTGCAGACGCGCTTAAACGGAGGGTGTCAAG	6930
QY	1618	AGCACGCCACCTGTAAAGATGACAGGCCCCGGGCAAGCAAGTGTGAGTGTAAAGTCACT	1677
Db	6931	AGCACGCCACCTGTAAAGATGACAGGCCCCGGGCAAGCAAGTGTGAGTGTAAAGTCACT	6990
QY	1678	ATGTCGGAGATGGGCTGAACTGTGAGCCGGAGAGCTGCCCATTTGACCGCTGTTCACGG	1737
Db	6991	ATGTCGGAGATGGGCTGAACTGTGAGCCGGAGAGCTGCCCATTTGACCGCTGTTCACGG	7050
QY	1738	ACAAATGCGAGTSCCAATGCAGACGCAAAATGTGTGACCTCCACTTCCAGGATACCACTG	1797
Db	7051	ACAAATGCGAGTSCCAATGCAGACGCAAAATGTGTGACCTCCACTTCCAGGATACCACTG	7110
QY	1798	TTGGGGTGTTCATCTACGCTCCCACTGGGCCAGTATAAGCTGACCTTTTGACAAAGCCA	1857
Db	7111	TTGGGGTGTTCATCTACGCTCCCACTGGGCCAGTATAAGCTGACCTTTTGACAAAGCCA	7170
QY	1858	GAGAGGCTGTGCCAAGCAAGCTGCCAACCATGGCAACCTACACCAAGCTCTCTATGCCC	1917
Db	7171	GAGAGGCTGTGCCAAGCAAGCTGCCAACCATGGCAACCTACACCAAGCTCTCTATGCCC	7230
QY	1918	AGAAGGCCAAGTACCACTGTGCTCAGCAGGCTGGCTGGAGACCGGCGGGTTGCCCTACC	1977
Db	7231	AGAAGGCCAAGTACCACTGTGCTCAGCAGGCTGGCTGGAGACCGGCGGGTTGCCCTACC	7290
QY	1978	CCAAGCTTTCGCTCCCAAGACTGTGGCTCTGGTGTGGTGGGATAGTGGACTATGGAC	2037
Db	7291	CCAAGCTTTCGCTCCCAAGACTGTGGCTCTGGTGTGGTGGGATAGTGGACTATGGAC	7350
QY	2038	CTAGACCCACACAGAGTGAAATGTGGATGTCTTCTGCTATCGATCGAAGATGTGAACT	2097
Db	7351	CTAGACCCACACAGAGTGAAATGTGGATGTCTTCTGCTATCGATCGAAGATGTGAACT	7400
QY	2098	GCACCTGCAAGGTGGGCTATGTGGGAGATGGCTTCTCATGCACTGGGGAACCTGCTGACGG	2157
Db	7401	-----	7400
QY	2158	TCCTGATGCTCTTCCCTCTACTCACAACCTTCTCTGACGGAAGTGTCTGGCTATTTCCACA	2217

QY	667	AGGTTTACGTGTGGATCTTCCACATCCACTGCCTGGGAAGACCCCTGCAAGGTTTCAGACG	726
Db	2765	AGGTTTACGTGTGGATCTTCCACATCCACTGCCTGGGAAGACCCCTGCAAGGTTTCAGACG	2824
QY	727	TGAGTGTGAAATGTGGAGCTGGCAGGGAATCGGTGACCTCTTCTGAAATGGCCAAACCT	786
Db	2825	TGAGTGTGAAATGTGGAGCTGGCAGGGAATCGGTGACCTCTTCTGAAATGGCCAAACCT	2884
QY	787	GCAGAAATGTGCAGCGGGAGCTCTTGTGTAACCTGGGTGTGGCCTTACGGCAATGACTGTTC	846
Db	2885	GCAGAAATGTGCAGCGGGAGCTCTTGTGTAACCTGGGTGTGGCCTTACGGCAATGACTGTTC	2944
QY	847	TGCTGATTCATCCCAACCTCGGGGGCGCTGTGACACCTTTACTACTTTTCGATCGCTCGS	906
Db	2945	TGCTGATTCATCCCAACCTCGGGGGCGCTGTGACACCTTTACTACTTTTCGATCGCTCGG	3004
QY	907	GGGAGTGTGGGAGCTGTCTCAATFACCTCCAGCTGCCCAAGGTGGAGTAAACCAAGGGTG	966
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QY	967	TGAAGCAGAAAGTCTCTACAACTGCTCCCTTCAAGAGGAACCTGGGAAGGCTGCCGGGAGC	1026
Db	3065	TGAAGCAGAAAGTCTCTACAACTGCTCCCTTCAAGAGGAACCTGGGAAGGCTGCCGGGAGC	3124
QY	1027	GGTGACGCTGGTGATACAGATCCCAAGTGTGCTGCAAGGGCTACTTCCGGCGAGACTGTTC	1086
Db	3125	GGTGACGCTGGTGATACAGATCCCAAGTGTGCTGCAAGGGCTACTTCCGGCGAGACTGTTC	3184
QY	1087	AGGCTGCCCTGGAGGACCAAGATGCCCTGTAAATAACCGGGGTGTCTGCTTTGATCAGT	1146
Db	3185	AGGCTGCCCTGGAGGACCAAGATGCCCTGTAAATAACCGGGGTGTCTGCTTTGATCAGT	3244
QY	1147	ACTCGGCAACCGGAGAGTGTAAATGCAACACCGGGCTTCAATGGGAAGGCGGTGTGAGATGT	1206
Db	3245	ACTCGGCAACCGGAGAGTGTAAATGCAACACCGGGCTTCAATGGGAAGGCGGTGTGAGATGT	3304
QY	1207	GCTGGCCGGGGAGATTTCGGGCTGATTGTCTGCCCTGTGGCTCTCAGACACGGACAGT	1266
Db	3305	GCTGGCCGGGGAGATTTCGGGCTGATTGTCTGCCCTGTGGCTCTCAGACACGGACAGT	3364
QY	1267	GCATGATGGCATCACGGGCTCCGGGAGTGCCTCTGTGAACCGGGGTGGACAGGCCCT	1326
Db	3365	GCATGATGGCATCACGGGCTCCGGGAGTGCCTCTGTGAACCGGGGTGGACAGGCCCT	3424
QY	1327	CGTGTGACACTCAGGACAGTTTCCCTGCAGTGTGTACGGCTCTCTGTTCTGCTCATGGCA	1386
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QY	1387	CCTGTAAGAGAAACAACACGTGTGAGTGTAACTCGGANTATGAAGGTGACGGAAATCACAT	1446
Db	3485	CCTGTAAGAGAAACAACACGTGTGAGTGTAACTCGGANTATGAAGGTGACGGAAATCACAT	3544
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Db	3545	GCAAGTGTGGATTTCTGCAAAACAGGACAAACCGGGGCTGTGCAAAAGGTGGCGAGATGCT	3604
QY	1507	CCAGAAAGGCAAGAGGTTCTCTGAGCTGCCAGAGGATCAAAAGGGGACGGGACCA	1566
Db	3605	CCAGAAAGGCAAGAGGTTCTCTGAGCTGCCAGAGGATCAAAAGGGGACGGGACCA	3664
QY	1567	GCTGCAACAGATAGACCCCTGTGCAACCGGCTTAAACGGAGGCTGTACAGACACGCCCA	1626
Db	3665	GCTGCAACAGATAGACCCCTGTGCAACCGGCTTAAACGGAGGCTGTACAGACACGCCCA	3724
QY	1627	CCTGTAAGATGACAGGCCCGGGCAAGCAAGTGTGAGTGTAAAGTCAATGTGCGAG	1686
Db	3725	CCTGTAAGATGACAGGCCCGGGCAAGCAAGTGTGAGTGTAAAGTCAATGTGCGAG	3784
QY	1687	ATGGGCTGAATGTGAGCGGAGCAGCTGCCATTGACCGCTTACAGGACAAATGGGC	1746
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QY	1747	AGTGCCATGCAGACGCCAAATGTGTGCACTCCACTTCCAGGATACCACTGTGGGGTGT	1806
Db	3845	AGTGCCATGCAGACGCCAAATGTGTGCACTCCACTTCCAGGATACCACTGTGGGGTGT	3904
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Db	3965	GTGCCAAAGAAAGCTGGACCATGGCAACCTCAACACAGCTCTCTCTATGCCAGAGGCCA	4024
QY	1927	AGTACCACCTGTGCTCAGCAGGCTGGCTGGAGACCGGGGGGTGCTTACCCACACAGCCT	1986
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QY	1987	TGCTTCCACAGAACTGTGTGCTCTGTGTGGTGTGGGATAGTGGACTATGACCTTAGACCCA	2046
Db	4085	TGCTTCCACAGAACTGTGTGCTCTGTGTGGTGTGGGATAGTGGACTATGACCTTAGACCCA	4144
QY	2047	ACAAGAGTCAAAATGTGGGATGTCTTCTGTCTATCGGATGAAAGATGTGAACCTGCACCTGCA	2106
Db	4145	ACAAGAGTCAAAATGTGGGATGTCTTCTGTCTATCGGATGAAAGATGTGAACCTGCACCTGCA	4204
QY	2107	AGGTGGGCTATGTGGGAGATGGCTTCTCATGAGTGGGAACTGTGTCAGGTCCTGATGT	2166
Db	4205	AGGTGGGCTATGTGGGAGATGGCTTCTCATGAGTGGGAACTGTGTCAGGTCCTGATGT	4264
QY	2167	CCTTCCCTCAGTCAAACTTCTGACCGGAAGTGTGGCTTATTCACACAGCTCAGCTC	2226
Db	4265	CCTTCCCTCAGTCAAACTTCTGACCGGAAGTGTGGCTTATTCACACAGCTCAGCTC	4324
QY	2227	GAGGCGTGCATTTCTAGAACACCTGACTGACCTGCCCTCCGCGGACCCCTCTTTGTGC	2286
Db	4325	GAGGCGTGCATTTCTAGAACACCTGACTGACCTGCCCTCCGCGGACCCCTCTTTGTGC	4384
QY	2287	CACAGAAACAGTGGGCTGGGGAGATGAGACCTTGTCTGGGGGGGACATCGAGCACACCC	2346
Db	4385	CACAGAAACAGTGGGCTGGGGAGATGAGACCTTGTCTGGGGGGGACATCGAGCACACCC	4444
QY	2347	TGCGCAATGTACGATGTTTTTTTCTACAATGACCTTGTCTCAATGGCACACCCCTGCAACGA	2406
Db	4445	TGCGCAATGTACGATGTTTTTTTCTACAATGACCTTGTCTCAATGGCACACCCCTGCAACGA	4504
QY	2407	GGGTGGGAAGCAGCTGCTCATCTGCCAGCCAGGACCCACCTCCAAACCGACGAGACCA	2466
Db	4505	GGGTGGGAAGCAGCTGCTCATCTGCCAGCCAGGACCCACCTCCAAACCGACGAGACCA	4564
QY	2467	GGTTTGTGATGGAAGAGCCATTTCTGAGTGGGACATCTTTGCTCCCAATGGGATCATTC	2526
Db	4565	GGTTTGTGATGGAAGAGCCATTTCTGAGTGGGACATCTTTGCTCCCAATGGGATCATTC	4624
QY	2527	ATGTCAATTTCCAGGCTTTAAAGACACCCCTGCCCGGTGACCTTGACCCACACTGGCT	2586
Db	4625	ATGTCAATTTCCAGGCTTTAAAGACACCCCTGCCCGGTGACCTTGACCCACACTGGCT	4684
QY	2587	TGGGAGCAGGAGTCTTTTGGCCATCATCTGTGTGACTGGGGCTGTTTGCCTTGGCTTGCCT	2646
Db	4685	TGGGAGCAGGAGTCTTTTGGCCATCATCTGTGTGACTGGGGCTGTTTGCCTTGGCTTGCCT	4744
QY	2647	ACTCTACTTTTCGGAATAAACCGGAGAACAAATCGGCTTCCAGCAATTTTGTAGTCGAGAGG	2706
Db	4745	ACTCTACTTTTCGGAATAAACCGGAGAACAAATCGGCTTCCAGCAATTTTGTAGTCGAGAGG	4804
QY	2707	ACATTAATGTTCAGCTCTTGGCAAGCAGCAGCTTGAGATATCTCGAACCCCTTGTATG	2766
Db	4805	ACATTAATGTTCAGCTCTTGGCAAGCAGCAGCTTGAGATATCTCGAACCCCTTGTATG	4864
QY	2767	AGAGCAAACTCAGCTCCCGGAGAACCTTCTTACGACCCCTTTCAGGACTCTGAGAAC	2826
Db	4865	AGAGCAAACTCAGCTCCCGGAGAACCTTCTTACGACCCCTTTCAGGACTCTGAGAAC	4924
QY	2827	GGCAGCTTGAAGGGCAATGACCCCTTGGAGGACACTGTGA	2864

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RESULT 10
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; Publication No. US20020197681A1
; GENERAL INFORMATION:
; APPLICANT: Weigel, Paul
; TITLE OF INVENTION: Identification of Hyaluronan Receptor for Endocytosis
; FILE REFERENCE: 5820.603
; CURRENT APPLICATION NUMBER: US/09/842,930A
; CURRENT FILING DATE: 2001-04-22
; PRIOR APPLICATION NUMBER: 60/245,320
; PRIOR FILING DATE: 2000-11-02
; PRIOR APPLICATION NUMBER: 60/199,538
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 4706
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-09-842-930A-1

Query Match 59.4%; Score 1936.8; DB 9; Length 4706;
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Matches 2402; Conservative 0; Mismatches 652; Indels 14; Gaps 6;

QY 11 GGAGCTTCCCAAGAACCCGAAACTTCCCGATTTCTTCCAGTTGCGAGGACATTTGCT 70
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QY 71 GAAAGATCTGCTGGCGCCAGGCGCCCTTCACTCTTTTGGACCTTTATCTGCGACCTTTTGA 130
Db 1455 CCGAGAGCTTGTGGACCTTGGCCCTTCACTGCTTGGCGCTTTGTCTAGTCTCTTCA 1514
QY 131 TGAGGAGCTCGGGTAAAGACTGGGACAAATACGGTTTAAATGCCCCAGGTTCTTCGGTA 190
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QY 191 CCATGCTGCTGCTGCGACCGCTGCTTCTGAAAACTTGAATGATCTCAATGCTAC 250
Db 1575 TCACCTGCTGCTGCGACCGCTGCTTGTGACAACTTAAAGTGAACCAAGTGCCAC 1634
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QY 551 GCCACCCGACCAAGCCCTCCATGCTGCTGCTGCTGAAACAGGACTTCTGTTCAACA 610
Db 1935 GCCTACGACCAAGCCCTTGGAAAGCTTGTGCCCCAGAGCAGCAGGACTTCTGTTCAATCA 1994
QY 611 AGACAACAGGACCAAGCTGAAAGGAGTATTTGAAGTTTTCATGTGATGAGATGCCAGGT 670
Db 1995 AGACAACAGGACCAAGCTGAAAGTCTTACTGAAAGTTCCAGTATCCAGTATCCAGGCT 2054

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Db 2115 TGTGAGGTTGTGAACTGGGAGTGACATCGGTGAGCTCTTTCTAAACGAAACAAATGTGAG 2174
QY 791 AATTGTGAGCGGGAGCTCTTCTTGGACCTGGGTGGGCTAGCGGATTCAGTGTCTGCT 850
Db 2175 AATTCAACACCGGGGACTCTTCTTGGAGCTGGGTATGGCTATGGCAATTCAGTGTCTACT 2234
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Db 2235 CATGAATCTTACCTAGTGGCGGATGTGACACTTTTACTACTTCTGATATTCGGGGGA 2294
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QY 1148 CTCGSCCACCAGAGAGTGTAAATGCAACACCGGCTTCAATGGAGCGGCTGTGATGTG 1207
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QY 1208 CTGGCGGGGAGATTCGGGCTGTGTTGCTGCTGCTGCTGCTCAGACCAAGGAGCTG 1267
Db 2595 CTGGCATGGAGATTTGGGCTGTGCTGTCAGCCCGCAGCTGCTCCGAGCATGGACAGTG 2654
QY 1268 CGATGATGGCATCAGGCTCCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1327
Db 2655 TGATGAGGAGATCAGAGCTCCGGGAGTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2714
QY 1328 GTGTGACACTCAGGAGTTTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1387
Db 2715 GTGTGACACTCCGAGCTGTATTGCGAGTGTGCAACCTGCTGCTGCTGCTGCTGCTGCTGCT 2774
QY 1388 CTGTAAGGAGAACACAGCTGTGAGTGTAACTCTGATTTATGAGTGTGAGTGTGAGTGTG 1447
Db 2775 CTGTACGGAGAACACAGCTGTGCTGTGTGTAACTTGTGACTGAGAGTGTGAGGATCAGATG 2834
QY 1448 CACAGTTGTGATTTCTGCAAAACAGGACCAACCGGGGCTGTGCAAAAGTGTGCAAGTGTGCT 1507
Db 2835 CACAGTGTGAGTTCTGCAAAACAGGACCAACCGGGGCTGTGCAAAAGTGTGCTGCTGCTGCTGCT 2894
QY 1508 CCAGAGGGCAGGAGGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1567
Db 2895 CCAGAGGGCAGGAGGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2954
QY 1568 CTGCACAGAGATGACCCCTGTGCGAGACGGGCTTTAAACGGAGGGTGTGCTGAGGAGCTGCT 1627
Db 2955 CTGCATAGAGATGACCCCTGTGCGAGAGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3014
QY 1628 CTGTAAAGATGACGGCCCGGGCAAGCAAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 1687
Db 3015 CTGCAGGATGACGGCCCGGGCAAGCAAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 3074
QY 1688 TGGGCTGACCTGTGAGCGGGAGGAGCTGCCCATTTGACGGCTGCTTACAGGACATGGGCA 1747
Db 3075 CGGAGTGGACTGTGAGCTTGAGCAGCTGCGGCTGCGAGCTGCGGCTGCGAGCTGCGGCTGCGAGCA 3134
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Db 1755 CAAGTTGCTGTCTCCCAAAACCTTGCTTATCACCCCCAAGATGCTTGGCAGGGTCTT 1814
QY 431 GCAAAATCTTACGACTTTGGCAACAAACAAATGGCTACATCAAAATTTAGCAACTTAATACA 490
Db 1815 GCAAAATCTTACTACAGTGGCAGCAAAACCCAGGATATACCAATTCAGCAAGTTGATACA 1874
QY 491 GCACTCAGGTTTGGCTGAGTGTATCAACCGATCCATCCACACCCAGTCACTCTCTTCG 550
Db 1875 GCACTCAGGCTTGGCTGTCAGTCACTCACTCACTCCATCCACACCCAGTCACTCTCTTCG 1934
QY 551 GCGCCACGACCAAGCCCTCCATGCCCTACCTGTAACCAACAGGACTTCTCTTCAACA 610
Db 1935 GCCTACGACAAAGCCCTGGAGCCCTTGCCCCAGAGCGAGGACTTCTCTGTTCAATCA 1994
QY 611 AGACAACAGGACAAAGCTGAAGGAGTATTTGAAGTTTCAATGTGATACGAGATGCCAAGT 670
Db 1995 AGACAACAGGACAAAGCTGAAGTCTTACCTGAAGTTCCACGTGATCCGAGACTCCAGAGC 2054
QY 671 TTTAGCTGTGGATCTCCACATCACTGCTGCGGAGACCCCTGCGAAGGTTCAAGCTGAG 730
Db 2055 TTTAGCTTCAGACCTCCCGAGTCTGCTTCTGGAAGACCCCTGCAAGGCTCAGAGCTGAG 2114
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QY 791 AATTGTGACGGGGAGCTCTTGTTGACCTGGGTGTGGCTTACGGCAATGACTGTCTGCT 850
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QY 851 GATTGATCCCACTGGGGGCGCTGTGACACTTTACTATCTTTCGATTCGCTCGGGGA 910
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QY 971 GCAGAAGTGTCTTCAAAACC---TGCCCTTCAAGAGGAACCTGGGAAGGCTGCCGGAGCG 1027
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QY 1088 GGCCTGCCCTGGAGGACAGATGCCCGCTGTAATAACCGGGGTGCTGCCTTGATCAGTA 1147
Db 2475 GGCCTGCCCTGGAGGACAGATACACCGTGTAAACCGGGGCATGTGCCGGGATCTGTA 2534
QY 1148 CTGGGCCACCGGAGAGTGTAAATGCAACACCGGCTTCAATGGGACGGGCTGTGAGATGTG 1207
Db 2535 CACACCCATGGGACAGTGCCTATGCCACACACCGGCTTCAACGGGACAGCTGCCAGCTCTG 2594
QY 1208 CTGGCGGGGAGATTCGGGCTGATGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1267
Db 2595 CTGGCATGGGAGATTTGGGCTGATGTGACGCCCGGAGCTGCTCCGAGCATGGACAGTG 2654
QY 1268 CGATGATGGCATCACGGGCTCGGGGCTGCTGCTGTAACCGGGGTGGACAGGCCCTC 1327
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QY 1328 GTGTGACACTCAGGAGTTTTGCCCTGCGAGTGTGACGCTCTCTTGTCTGCTATGCCAC 1387
Db 2715 GTGTGACACTCCCAAGCTGATTCGACAGTGTGCACACCTGTTGCTCCGTCAGCGCAC 2774
QY 1388 CTGTAAGGAGAACACAGTGTGAGTGTAACTCGAATATGAGGTGACGGAATCAATG 1447
Db 2775 CTGTACGAGAACACACAGTGTGTGTAACTTGAACTACGAAGGTGACGGGATCAATG 2834
QY 1448 CACAGTGTGTGATTTCTCAAAACAGCAACCGGGGCTGTGCAAGGTGGCCAGATGCTC 1507
Db 2835 CACAGTGTGTGACTTCTGCAAAACAGCAACCGGGGCTGTGCGAAGGTGCTTAAGTGTCTC 2894

QY 1508 CCAGAAGGGCACGAAGGTCTCTCTGAGCTGCCAGAAGGATACAAAGGGGACGGGCACAG 1567
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Db 3255 TGCCAAACGAAGCTGGACCATAGCCACCTACAACAGCTCTCTATGCCAGAGGCCAA 3314
QY 1928 GTACACCTGTGTGACAGCTGGCTGGAGACCGGGGGTGTGCTATCCCCACAGCCTT 1987
Db 3315 GTATCACCTGTGTGCGCGCTGGCTGGAGAGTGGCGGGTGGCTACCCGACTACGTA 3374
QY 1988 CGCCTCCAGAACCTGTGGCTCTGGTGTGGTGGGATGTGAGCTATGACACTAGACCCAA 2047
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QY 2108 GGTGGCTATGTGGAGATGGCTTCTCATGAGTGGGAACTGTGTGAGGTCTGTATGTC 2167
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QY 2288 ACAGAACAGTGGGCTGGGGAGATGAGACTGTGTGGGGGGGACATTCGAGACCACT 2347
Db 3675 ACAGAACAGTGGGCTACCGGGAATTAAGAGCTGTGTGCGGGGACATTCGAGACCACT 3734
QY 2348 CGCCAAATGTGACATGTTTTTCTAATGACTTGTCAATGGCACCCCTGCAACAG 2407
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Db 3795 GCTGGGAGCAACTGTCTCATTTACCTTCAGCCAGGACCGAGCTCCACC---AAGAGACAG 3851
QY 2468 GTTGTGTGATGGAAGACCAATTTGACAGTGGGACATCTTGTCCCTCCAAATGGGATCAT 2527
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QY 2528 TGTCAATTTCCAGGCTTTAAAGCACCCCTGCCCCCGTGTGACCTTGACCCACATCGCTT 2587
Db 3912 TATTATTCTGAACCTTTGAGAGCTCTCTCCCAACGCGACCAACGGCTGCCCACTCTGSCCT 3971

QY 2588 GGGAGCAGGATCTCTTTGGCCATCATCTGGTGAAGTGGGGCTGTGCTGGCTGCTTA 2647
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Db 3972 GGGGACAGATATATCTGTGCGCTGTCTGTGCTACTGTGTGGATGTCTTGGCAGCTTA 4031
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QY 2648 CTCCTACTTTCGGATAAACCAGAGAACAAATCGGCTTCCAGCAATTTTGGTCCGGAAGAGGA 2707
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Db 4091 CATTTGATGTCTTTGGCTTTTGGCAAGCAGCAGCCCAAGAAATATCGCAAAACCTCTGTATGA 4150
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QY 2828 GCAGCTTGAGGCAATACCCCTTGGAGACACTGTGAGGCGCTTGGACGGAGATGCCAGC 2887
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QY 2888 CATCACTACTGCCACCTGGGCAATCACTGTGATTTCTCAGC---ACCAGTTGCCCTTT 2944
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QY 2945 AGCAACGTAAGTCTCTTAAGCACTCAGAAAGCAATACCTCATCTCTCTGGCTGATCTGGG 3004
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QY 3005 GGTGTTTCTGTGGGTGAGAGATGTGTG-CTGTGCCCAACCGAGTACAGCTTCTCTCTCT 3063
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Db 4388 ATTGTCCGCGAGGCTAAGGAGCCATGTTGCTGTGATACCTGGGGGACCTCCACCTCTCT 4447
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QY 3064 GACCCCTTT 3071
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Db 4448 GAGCCTAT 4455
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RESULT 12

US-10-023-896-38
; Sequence 38, Application US/10023896
; Publication No. US2003002776A1

; GENERAL INFORMATION:
; APPLICANT: Victor Roschke
; TITLE OF INVENTION: 29 Human Cancer Associated Proteins
; FILE REFERENCE: PA004P1
; CURRENT APPLICATION NUMBER: US/10/023,896
; PRIOR FILING DATE: 2001-12-21
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: unassigned
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: PCT/US00/23794
; PRIOR FILING DATE: 2000-08-30
; PRIOR APPLICATION NUMBER: 60/152,296
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: 60/158,003
; PRIOR FILING DATE: 1999-10-06
; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 38
; LENGTH: 718
; TYPE: DNA
; ORGANISM: Homo sapiens

US-10-023-896-38

Query Match 21.7%; Score 708; DB 15; Length 718;
Best Local Similarity 99.9%; Pred. No. 9.3e-213;
Matches 708; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2552 ACCCCCTGCCCGCTGACCTTGACCCACACTGGCTTTGGGAGCAGGATCTCTTTGCCAT 2611
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Db 9 ACCCCCTGCCCGCTGACCTTGACCCACACTGGCTTTGGGAGCAGGATCTCTTTGCCAT 68
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QY 2612 CATCTGGTGAAGTGGGGCTGTGCTTGGCTTACTCTTACTTTGGATTAACCGGAG 2671
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Db 69 CATCTGGTGAAGTGGGGCTGTGCTTGGCTTACTCTTACTTTTCGGATAAACCGGAG 128
QY 2672 RACATCGCTTCCAGCATTTTGGTCCGAAAGAGACATTAATGTTGCAGCTCTTTGGCAA 2731
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Db 129 AACATCGCTTCCAGCATTTTGGTCCGAAAGAGACATTAATGTTGCAGCTCTTTGGCAA 188
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QY 2732 GCAGCAGCTGAGAAATATCTCGAACCCCTTGTATGAGAGCACAACCTCAGCTCCGCCAGA 2791
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Db 189 GCAGCAGCTGAGAAATATCTCGAACCCCTTGTATGAGAGCACAACCTCAGCTCCGCCAGA 248
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QY 2792 ACCTTCTACGACCCCTTCAAGCACTCTGAGAAAGAGAGCTTGGGGCAATGACCCCTT 2851
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Db 249 ACCTTCTACGACCCCTTCAAGCACTCTGAGAAAGAGAGCTTGGGGCAATGACCCCTT 308
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QY 2852 GAGGACATGTGAGGGCTTGGACGGGAGATGCCAGCATCACTCACTGCCACCTGGGCCA 2911
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Db 309 GAGGACATGTGAGGGCTTGGACGGGAGATGCCAGCATCACTCACTGCCACCTGGGCCA 368
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QY 2912 TCAACTGTGAATTTCTCAGCACCAGTTGCCCTTTTAGGAAAGTAAAGTCTTTAAGCACTCA 2971
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QY 2972 GAAGCATACTCATCTCTCTGCTGATCTGGGGTGTGTTCTGTGGGTGAGAGATGTGT 3031
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Db 429 GAAGCATACTCATCTCTCTGCTGATCTGGGGTGTGTTCTGTGGGTGAGAGATGTGT 488
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QY 3032 TCGTGTGCCACCCAGTACAGCTTCTCTCTGACCCCTTGGCTCTTCTCTCTTGTACT 3091
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Db 489 TCGTGTGCCACCCAGTACAGCTTCTCTCTGACCCCTTGGCTCTTCTCTCTTGTACT 548
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QY 3092 CTTAGCTGGCACTGCTCTCAATTTCTGCCCTCATCATGATGGGTAACTGTGATCTTCTCC 3151
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Db 549 CTTAGCTGGCACTGCTCTCAATTTCTGCCCTCATCATGATGGGTAACTGTGATCTTCTCC 608
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QY 3152 TGTAGATGTGAAGCTCTCTCTTGTATCCAGCCCTTAGCCAGTGTGTCACACAGA 3211
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Db 609 TGTAGATGTGAAGCTCTCTCTTGTATCCAGCCCTTAGCCAGTGTGTCACACAGA 668
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QY 3212 ACTGTGCACATAAAGGTTTATGGAACAGAAAAA 3260
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Db 669 ACTGTGCACATAAAGGTTTATGGAACAGAAAAA 717
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RESULT 13

US-09-822-830A-559
; Sequence 559, Application US/09822830A
; Patent No. US20020142952A1
; GENERAL INFORMATION:
; APPLICANT: Genetics Institute, Inc.
; APPLICANT: Wong, Gordon G.
; APPLICANT: Clark, Hilary
; APPLICANT: Fechtel, Kim
; APPLICANT: Agostino, Michael J.
; APPLICANT: Howes, Steven H.
; APPLICANT: Resnick, Richard J.
; APPLICANT: Gulukota, Kamalakar
; APPLICANT: Graham, James R.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
; FILE REFERENCE: GIN 6402
; CURRENT APPLICATION NUMBER: US/09/822,830A
; CURRENT FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/195,604
; PRIOR FILING DATE: 2000-04-06
; NUMBER OF SEQ ID NOS: 631
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 559
; LENGTH: 722
; TYPE: DNA
; ORGANISM: Homo sapiens

US-09-822-830A-559

Query Match 16.5%; Score 537; DB 9; Length 722;
Best Local Similarity 99.6%; Pred. No. 1.4e-158;

Matches	548;	Conservative	0;	Mismatches	1;	Indels	1;	Gaps	1;
Qy	2695	AGTCGGAAGAGGACATTAATGTTGCAGTCTTTGGCAAGCAGCAGCCCTGAGAAATATCTCGA	2754						
Db	172	AGTCGGAAGAGGACATTAATGTTGCAGTCTTTGGCAAGCAGCAGCCCTGAGAAATATCTCGA	231						
Qy	2755	ACCCCTTTGTATGAGAGCACAACCTCAGTCTCCCCAGAAACCTTCTCTACGACCCCTTTCACGG	2814						
Db	232	ACCCCTTTGTATGAGAGCACAACCTCAGTCTCCCCAGAAACCTTCTCTACGACCCCTTTCACGG	291						
Qy	2815	ACTCTGAAGAACGGCAGCTTGAGGGCAATGACCCCTTGAGGACACTGTGAGGGCCCTGGAC	2874						
Db	292	ACTCTGAAGAACGGCAGCTTGAGGGCAATGACCCCTTGAGGACACTGTGAGGGCCCTGGAC	351						
Qy	2875	GGGAGATGCCAGCCATCACTCACTGCCACCTGGGCCATCAACTGTGAATTTCTCAGACACCA	2934						
Db	352	GGGAGATGCCAGCCATCACTCACTGCCACCTGGGCCATCAACTGTGAATTTCTCAGACACCA	411						
Qy	2935	GTTCGCTTTTAGGAACTGAAGTCTTTAAGCACTCAGAGGCCAATCCTCATCTCTCTGG	2994						
Db	412	GTTCGCTTTTAGGAACTGAAGTCTTTAAGCACTCAGAGGCCAATCCTCATCTCTCTGG	471						
Qy	2995	CTGATCTGGGGGTGTGTTCTGTGGTGCAGAGATGTGTTGTCGTGCCACCCAGTCAGACT	3054						
Db	472	CTGATCTGGGGGTGTGTTCTGTGGTGCAGAGATGTGTTGTCGTGCCACCCAGTCAGACT	531						
Qy	3055	TCTCTCTGACCCCTTTGGCTCTTCTCTTTGTACTCTTCAGTGTGSCACTGCTCCATT	3114						
Db	532	TCTCTCTGACCCCTTTGGCTCTTCTCTTTGTACTCTTCAGTGTGSCACTGCTCCATT	591						
Qy	3115	CTCGCCTACATGATGGGTAACTGTGATCTTTCTCCCTGTTAGATTGTAAGCCTCCTCT	3174						
Db	592	CTCGCCTACATGATGGGTAACTGTGATCTTTCTCCCTGTTAGATTGTAAGCCTCCTCT	651						
Qy	3175	TTGTATCCCCAG - CCCCTAGGCCAGTGCCTGCACACAGGAACCTGTGCAATAAAGGTTTAT	3233						
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Qy	3234	GGAAACAGAA 3243							
Db	712	GGAAACAGAA 721							

RESULT 14	
US-10-264-237-1320	
Sequence 1320, Application US/10264237	
Publication No. US20040009491A1	
GENERAL INFORMATION:	
APPLICANT: Birse et al.	
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies	
FILE REFERENCE: PA131P1	
CURRENT APPLICATION NUMBER: US/10/264,237	
CURRENT FILING DATE: 2002-10-04	
PRIOR APPLICATION NUMBER: PCT/US01/16450	
PRIOR FILING DATE: 2001-05-18	
PRIOR APPLICATION NUMBER: US 60/205,515	
PRIOR FILING DATE: 2000-05-19	
NUMBER OF SEQ ID NOS: 2876	
SOFTWARE: PatentIn Ver. 3.1	
SEQ ID NO 1320	
LENGTH: 3681	
TYPE: DNA	
ORGANISM: Homo sapiens	
FEATURE:	
NAME/KEY: misc feature	
LOCATION: (5)..(5)	
OTHER INFORMATION: n equals a,t,g, or c	
FEATURE:	
NAME/KEY: misc_feature	
LOCATION: (7)..(7)	
OTHER INFORMATION: n equals a,t,g, or c	
FEATURE:	
NAME/KEY: misc_feature	

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; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; PRIOR FILING DATE: 2001-07-30
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; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
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GenCore version 5.1.6
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Listing first 45 summaries

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DEFINITION Sequence 210 from Patent WO02059315.
ACCESSION AX686401
VERSION AX686401.1
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS Shimkets, R.A., Patturajan, M., Vernet, C.A., Casman, S.J.,
Malyankar, U., Shenoy, S., Spytek, K.A., Gangolli, E., Miller, C.,
Boldog, F., Li, L., Taupier, R.J., Kekuda, R., Smithson, G.,

AX686401 3260 bp DNA linear PAT 29-MAR-2003

Zerhusen, B. D., Liu, X., Colman, S. D., Tchernev, V., Si, J., Edinger, S.,
Stone, D., Sciore, P., Millet, I., and Rothenberg, M.
Human nucleic acids and polypeptides and methods of use thereof
Patent: WO 02059315-A 210 01-AUG-2002;
Curagen Corporation (US)

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Matches 3260; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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FEATURES
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STAB2 gene; stabilin-2.
Homo sapiens (human)
Homo sapiens
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1 Politz,O., Gratchev,A., McCourt,P.A.G., Schledzewski,K., Guillot,P.,
Johansson,S., Svineng,G., Franke,P., Kannicht,C., Kzhyshkowska,J.,
Longati,P., Velten,F.W., Johansson,S. and Goerd,S.
Stabilin-1 and -2 constitute a novel family of fasciclin-like
hyaluronan receptor homologues
Biochem. J. 362 (Pt 1), 155-164 (2002)
21818465
11829752
2 Politz,O., Gratchev,A., McCourt,P.A.G., Schledzewski,K.,
Guillot,P., Johansson,S., Birk,R., Hakiy,N., Franke,P., Kodelja,V.,
Kannicht,C., Orfanos,C.E., Johansson,S. and Goerd,S.
Stabilin-1 and stabilin-2 constitute a novel family of fasciclin
domain-containing adhesion molecules associated with
endothelial-macrophage differentiation and angiogenic processes
Unpublished
3 (bases 1 to 8266)
Gratchev,A.
Direct Submission
Submitted (27-JUL-2000) Gratchev A., Department of Dermatology,
University Medical Center Mannheim, Theodor-Kutzer-Ufer 1, D-68135
Mannheim, GERMANY
Revised by author 27-APR-2001
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gene

CDS

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ORIGIN

Query Match		99.4%;	Score 3241.4;	DB 9;	Length 8266;
Best Local Similarity		99.7%;	Pred. No. 0;		
Matches 3245;		Conservative 1;	Mismatches 8;	Indels 0;	Gaps 0;
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DB	5705	TGAGTGTGAAATGTGGAGCTGGCAGGGAATCGGTGACCTCTTTCTGAATGGCCAAACCT	5764
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ORIGIN

Query Match	99.2%; Score 3234.2; DB 9; Length 8251;
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Db	7643	ACTCCTACTTTTCGGATAAAACCGGAGAAACAATCGCGCTTCCAGACATTTTGTAGTCGGAAAGAGG	7702
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Db	7703	ACATTAATGTTGACAGCTCTTGGGCAAGCAGCAGCCTGAGAAATATCTCGAAACCCCTTGTATG	7762
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Qy	2947	GAACGTAAGTCCCTTTAAGCACTCAGAGCCATACCTCATCTCTGGCTGATCTGGGG	3006
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LOCUS	Homo sapiens mRNA for FLJ00122	protein.	PRI 15-FEB-2002
DEFINITION			
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VERSION	AK074051.1	GI:18676449	
KEYWORDS	fls (full insert sequence).		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE	1		
AUTHORS	Jikuya,H., Takano,J., Nomura,N., Kikuno,R., Nagase,T. and Ohara,O.		
TITLE	The nucleotide sequence of a long cDNA clone isolated from human spleen		
JOURNAL	Published Only in Database (2002)		
REFERENCE	2	(bases 1 to 5604)	
AUTHORS	Jikuya,H., Takano,J., Nomura,N., Kikuno,R., Nagase,T. and Ohara,O.		
TITLE	Submitted (21-JAN-2002) Takahiro Nagase, Kazusa DNA Research Institute, Department of Human Gene Research; 1532-3, Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:cdnainfo@kazusa.or.jp, URL:http://www.kazusa.or.jp/NEDO, Tel:81-438-52-3913, FAX:81-438-52-3914)		
JOURNAL			
COMMENT	NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert and 5'- &		

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RESULT 6
AK024503

LOCUS AK024503 4575 bp mRNA linear PRI 29-SEP-2000
DEFINITION Homo sapiens mRNA for FLJ00112 protein, partial cds.
ACCESSION AK024503
VERSION AK024503.1 GI:10440525
KEYWORDS fis (full insert sequence).
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 4575)

AUTHORS Ohara,O., Nagase,T., Kikuno,R. and Okumura,K.
 TITLE The nucleotide sequence of a long cDNA clone isolated from human spleen
 JOURNAL Published Only in DataBase (2000)
 REFERENCE 2 (bases 1 to 4575)
 AUTHORS Ohara,O., Nagase,T., Kikuno,R. and Okumura,K.
 TITLE Direct Submission
 JOURNAL Submitted (24-AUG-2000) Osamu Ohara, Kazusa DNA Research Institute, Department of Human Gene Research; 1532-3, Yana, Kisarazu, Chiba 292-0812, Japan [E-mail:cdnaiffo@kazusa.or.jp, URL:http://www.kazusa.or.jp/NEDO, Tel:81-438-52-3913, Fax:81-438-52-3914]
 COMMENT NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5'- and 3'-end one pass sequencing and clone selection: Kazusa DNA Research Institute.
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ORIGIN

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 2047 TGAGTGTGAAATGTGGAGCTGGCAGGACATCGGTGACCTCTTCTTGAATGGCCAAACCT 2106
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DEFINITION Homo sapiens mRNA for FELE-2, complete cds.
ACCESSION AB052958
VERSION AB052958.1 GI:22779440
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

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JOURNAL

Adachi, H. and Tsujimoto, M.
FEE-1, a novel scavenger receptor with in vitro bacteria-binding
and angiogenesis-modulating activities
J. Biol. Chem. 277 (37), 34264-34270 (2002)
2206516
12071138

FEATURES

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Adachi, H. and Tsujimoto, M.
FEE-1, a novel scavenger receptor with in vitro bacteria-binding
and angiogenesis-modulating activities
J. Biol. Chem. 277 (37), 34264-34270 (2002)
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VERSION AY227444.1 GI:28848629
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SOURCE Homo sapiens (human)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 4492)
AUTHORS Zhou, B., McGary, C.T., Weigel, J.A., Saxena, A. and Weigel, P.H.
TITLE Purification and molecular identification of the human hyaluronan
receptor for endocytosis
JOURNAL Glycobiology 13 (5), 339-349 (2003)
MEDLINE 22588541
PUBMED 12626425
REFERENCE 2 (bases 1 to 4492)
AUTHORS Weigel, P.H.
TITLE Direct Submission
JOURNAL Submitted (29-JAN-2003) Biochemistry and Molecular Biology,
University of Oklahoma Health Sciences Center, BMSB Room 860,
Oklahoma City, OK 73104, USA
Location/Qualifiers

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VERSION AL133021.1 GI:6453577
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SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 3642)
AUTHORS Blum, H., Bauersachs, S., Mewes, H.W., Gassenhuber, J. and Wiemann, S.
TITLE Direct Submission
JOURNAL Submitted (15-NOV-1999) MIPS, Am Klopferspitz 18a, D-82152
Martinsried, GERMANY
COMMENT Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by LMU (Ludwig Maximilians University, Munich/Germany) within the cDNA sequencing consortium of the German Genome Project.
This clone (DKFZp434E0321) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzd.de Further information about the clone and the sequencing project is available at <http://www.mips.biochem.mpg.de/proj/cDNA/>.

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REFERENCE 1
AUTHORS Shimkets, R.A., Patturajan, M., Vernet, C.A., Casman, S.J.,
Malyan, U., Shenoy, S., Spytek, K.A., Gangolli, E., Miller, C.,
Bodog, F., Li, L., Taupier, R.J., Kekuda, R., Smithson, G.,
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Curagen Corporation (US)
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Db	5611	ATAATAAGGCTAAGATCATATCCAGTGTATCATCAGTACTAATGGGATTTGTATATCA	5670	QY	1438	GAATCACATGACAGTGTGATTTCTGCAACACAGGCAACCGGGGCTGTGCAAGGTG	1497
QY	367	TAGACAAATGCTATCTCCAAAATTTGCTTATCACTCCCAAGACACTCTGGAGNA	426	Db	6751	GAATCACATGACAGTGTGATTTCTGCAACACAGGCAACCGGGGCTGTGCAAGGTG	6810
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LOCUS AX149461 3625 bp DNA linear PAT 08-JUN-2001
DEFINITION Sequence 17 from Patent WO0136638.
ACCESSION AX149461
VERSION AX149461.1 GI:14347936
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Shimketa, R.A., Lichenstein, H., Vernet, C. and Fernandes, E.
TITLE Polypeptides and nucleic acids encoding same
JOURNAL Patent: WO 0136638-A 17 25-MAY-2001;
Curagen Corporation (US)
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/db_xref="taxon:9606"
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LOCUS AY007370 4706 bp mRNA linear ROD 23-OCT-2002
DEFINITION Rattus norvegicus hyaluronan receptor for endocytosis HARE.
ACCESSION AY007370
VERSION AY007370.1 GI:24285892
KEYWORDS Rattus norvegicus (Norway rat)
SOURCE Rattus norvegicus
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Rattus.
REFERENCE 1 (bases 1 to 4706)
AUTHORS Zhou, B., Weigel, J.A., Saxena, A. and Weigel, P.H.
TITLE Molecular Cloning and Functional Expression of the Rat 175-kDa
Hyaluronan Receptor for Endocytosis
JOURNAL Mol. Biol. Cell 13 (8), 2853-2868 (2002)
MEDLINE 22169209
PUBMED 12181351
REFERENCE 2 (bases 1 to 4706)
AUTHORS Zhou, B., Weigel, J.A. and Weigel, P.H.
TITLE Direct Submission
JOURNAL Submitted (23-AUG-2000) Department of Biochemistry and Molecular
Biology, University of Oklahoma Health Sciences Center, 940 Stanton
L. Young, BMSB 860, Oklahoma City, OK 73104, USA
Location/Qualifiers
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33 39.4 1.2 855 6 5223394-3 Patent No. 5223394
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36 39.4 1.2 863 2 US-08-459-657-11 Sequence 11, Appl
37 39.4 1.2 863 2 US-08-460-132-11 Sequence 11, Appl
38 39.4 1.2 863 5 PCT-US92-02050-11 Sequence 11, Appl
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ALIGNMENTS

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; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Sealhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304

COMPUTER READABLE FORM:
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 230:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1482 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: SPLN004
; CLONE: 1561663

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QY	2133	TCATG	CAGTGGG	AACTGCTG	CAAGTCC	TGATGTCT	TCCCTCA	CTCACA	AACTTCC	CTG	2192
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QY	2193	ACGGA	AGTGTGG	CTATTC	CAACAG	CTC	AGCTGAG	CGCGTGC	ATTTCTAG	AACACCTG	2252
Db	546	GGGAT	GCTATT	TGGCTAT	TGCCAAT	GCAC	CCAGCGGG	GTCTCG	AACTTCTC	TGGACTTCC	605
QY	2253	ACTG	ACCTGTCC	ATCCGG	GCAC	CCCTTTGT	GC	CAGACAGTGG	CGCTGGG	GAGAA	2312
Db	606	GATG	ATGAGCTC	AGTATA	AGACACT	CTTGT	CTCCTGTCA	ATGAAG	CTTTG	TGGACAC	665
QY	2313	GAGAC	CTTGTCTGG	GGGCACTCG	AGCA	CCACCTCG	CCCAATGT	TCAGCA	TGTTTTTCTAC	2372	
Db	666	ATGA	CGCTGAGTGG	CGCCAG	ACTTGG	AGTGCAT	GCCTCC	AAAGCC	ACCCTCTTA	AGTGCC	725
QY	2373	AATG	ACCTTGTCA	ATGG	CA	CCCTGCA	ACGAGGTGG	GAAGCA	AGTGTCTCAT	CACT	2432
Db	726	AA	CGCCAG	CGGGAGT	TGCTTCCG	CGCCCACTCAG	GCCTC	ATCAT	CAGTGC	AG	785
QY	2433	CCG	AGCCAG	GACC-----	CACTC	CAACG	AGGAG	CCAGGTGT	TGTGATGG	AGAGCC	2486
Db	786	GCAG	GCCTTG	CAACAG	TTCTCT	GGGCCCTGTG	CGCC	CAAGG	ACAGTGTG	GTGACCGT	845
QY	2487	ATTCT	G	AGTGGG	ACATCTT	TGGCTCCAA	TGGGATCA	TTATG	ATTCATTT	CCAGG	2546
Db	846	ATCAT	TGTGG	GACATCAT	GGCCCTCA	TGGCAT	CTCA	TGGCAT	CTCCATG	CTCTGG	905
QY	2547	AAAG	CA	CCCCCTG	CCCCG	TG	ACCTTG	2573			
Db	906	CTGG	CA	CCCCC	CACAG	CCCCC	AGG	CA	GTG	932	

RESULT 2:

US-09-833-381-1252
; Sequence 1252, Application US/09833381
; Patent No. 6672186
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.

```

; TITLE OF INVENTION: No. 6672186el Nucleic Acid and Protein Homologs
;
; FILE REFERENCE: 5800-119
; CURRENT APPLICATION NUMBER: US/09/833,381
; CURRENT FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 09/516,448
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 2050
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1252
; LENGTH: 409
; TYPE: DNA
; ORGANISM: Homo sapiens
;
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(409)
; OTHER INFORMATION: n = A,T,C or G
; US-09-833-381-1252

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	Query Match	3.3%;	Score 107.2;	DB 4;	Length 409;
	Best Local Similarity	56.3%;	Pred. No. 1.2e-21;		
	Matches 218;	Conservative 0;	Mismatches 166;	Indels 3;	Gaps 1;
Qy	1452	GTGTGCGATTTCTGCAAAACAGGACAAACGGGGGCTGTGCAAAAGTGGCCAGATGCTCCCGAG	1511		
Dd	23	GTGCGCGANCTGTGCCAAGAGGGGCATGTGTGGCTGCAGTAAAGCATGCCAACTGCGACCCAG	82		
Qy	1512	AAGGGCACGAAAGTCTCTTGCAGCTGCCAAGAGGGGATCAAAAGGGGACGGGCACAGCTGC	1571		
Dd	83	GTGGGGCACAGTGTGTTGGTTGCACCTGCTGCCTGCACTATGAGGGTGCAGGTTTGGAGCTGC	142		
Qy	1572	ACAGCATAGACCCCTGTGCAGACGGCCCTTAAACGGAGGGTGTCACGAGCAGCCACCTGT	1631		
Dd	143	CGAGCTCGAGACCCCTGCTTGGATGTCGCCACCGTGGAGGGTTGCAGCGAGCAGCTGACTGC	202		
Qy	1632	AAGATGACAGGCCCGCGCAAGCAAAAGTGTGAGTGTAAAGTCACTATGTCGGAGATGGG	1691		
Dd	203	CTCAAATACCGTTCGAAACACACGGCGCTGTGAATGCCACGTAGGCTACGTGGGTGATGGG	262		
Qy	1692	CTGAACTGTGAGCCGGAGC---AGCTGCCCATTGACCGCTGCTTACAGGACAATGGGCAG	1748		
Dd	263	CTGCAGTGTCTANAGGAGCTTGAACCCCTGTGCGACAGATGCTTTGGAGGATCATCACCT	322		
Qy	1749	TGCCATGACAGCGCAAAATGTGTGCACTCTCACTTCCAGGATACCACTGTGGGGGTGTC	1808		
Dd	323	TGCCCACTGATGCTTTGTGCATGACCTACATTTCCAGGAAAAACAGGCTGGTGTCTTC	382		
Qy	1809	CATCTAGCTCCCCACTGGGCCAGTAT	1835		
Dd	383	CACATCCAGGCCACCACTGGCCCTTAT	409		

RESULT 3

```

US-08-024-868-1
; Sequence 1, Application US/08024863
; Patent No. 5386013
; GENERAL INFORMATION:
; APPLICANT: Lee, Tae Ho
; APPLICANT: Wisniewski, Hans Georg
; APPLICANT: Wilcek, Jan
; TITLE OF INVENTION: Cytokine-Induced Protein, TSG-6, DNA
; TITLE OF INVENTION: Coding Thereof and Uses Thereof
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brody and Neimark
; STREET: 419 Seventh Street, NW
; CITY: Washington
; STATE: DC
; COUNTRY: US
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

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SOFTWARE: Patent In Release #1.24
CURRENT APPLICATION DATA: US/08/024,868
FILING DATE: 13-MAY-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/642,312
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Livnat, Shmuel
REGISTRATION NUMBER: 33,949
REFERENCE/DOCKET NUMBER: VILCEK=1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-628-5197
TELEFAX: 212-737-3528
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1414 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
CELL TYPE: Fibroblast
CELL LINE: FS-4
FEATURE:
NAME/KEY: CDS
LOCATION: 69..899
OTHER INFORMATION:
US-08-024-868-1

Query Match 2.5%; Score 81.4; DB 1; Length 1414;
Best Local Similarity 55.5%; Pred. No. 1.3e-13;
Matches 157; Conservative 0; Mismatches 126; Indels 0; Gaps 0;

QY 1795 CTGTGGGGTGTTCATCTACGCTCCCACTGGGCGCAGTATAGCTGACCTTTGACAAAG 1854
Db 169 CAGCGGTGTGTACACAGAGAGACGGTCTGGCAATATACAGCTACCTACGAGAG 228
QY 1855 CCAGAGAGCGCTGTGCCAAGAGTGGCACTTACCAACAGCTCTCTCTATG 1914
Db 229 CTAAGCGGTGTGTGAATTTGAAGCGGCCCATCTCGCAACTTACAGCAGCTAGAGGAG 288
QY 1915 CCCAGAGCGCCAAAGTACCACTGTGCTCAGCAGGCTGGCTGGAGCGGGGGTTCCT 1974
Db 289 CCAGAAAATTTGGATTTTCATGCTGTGCTGGATGGATGGCTAAAGGCGAGAGTTGGAT 348
QY 1975 ACCCCACAGCCTTCGCCCTCCAGAACTGTGCTCTGTGTTGGGATAGTGACTATG 2034
Db 349 ACCCATTTGTGAAGCGCGGCCCACTGTGGATTTGAAAACCTGGCATTTATTGATTATG 408
QY 2035 GACCTAGACCCCAACAGAGTGAATGTGGGATGCTTCTGCTA 2077
Db 409 GAATCCGCTCTCAATAGGAGTGAAGATGGGATGCTATTGCTA 451

RESULT 4

US-08-242-097-1
Sequence 1, Application US/08242097
Patent No. 5846763
GENERAL INFORMATION:
APPLICANT: Lee, Tae Ho
APPLICANT: Wisniewski, Hans Georg
APPLICANT: Vilcek, Jan
TITLE OF INVENTION: Cytokine-Induced Protein, TSG-6, DNA Coding
TITLE OF INVENTION: Therefor and Uses Thereof
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.

ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/242,097
FILING DATE: 13-MAY-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Browdy, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: LEE26/VILCEK=1B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-628-5197
TELEFAX: 212-737-3528
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1414 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
CELL TYPE: Fibroblast
CELL LINE: FS-4
FEATURE:
NAME/KEY: CDS
LOCATION: 69..899
OTHER INFORMATION:
US-08-242-097-1

Query Match 2.5%; Score 81.4; DB 2; Length 1414;
Best Local Similarity 55.5%; Pred. No. 1.3e-13;
Matches 157; Conservative 0; Mismatches 126; Indels 0; Gaps 0;

QY 1795 CTGTGGGGTGTTCATCTACGCTCCCACTGGGCGCAGTATAGCTGACCTTTGACAAAG 1854
Db 169 CAGCGGTGTGTACACAGAGAGACGGTCTGGCAATATACAGCTACCTACGAGAG 228
QY 1855 CCAGAGAGCGCTGTGCCAAGAGTGGCACTTACCAACAGCTCTCTCTATG 1914
Db 229 CTAAGCGGTGTGTGAATTTGAAGCGGCCCATCTCGCAACTTACAGCAGCTAGAGGAG 288
QY 1915 CCCAGAGCGCCAAAGTACCACTGTGCTCAGCAGGCTGGCTGGAGCGGGGGTTCCT 1974
Db 289 CCAGAAAATTTGGATTTTCATGCTGTGCTGGATGGATGGCTAAAGGCGAGAGTTGGAT 348
QY 1975 ACCCCACAGCCTTCGCCCTCCAGAACTGTGCTCTGTGTTGGGATAGTGACTATG 2034
Db 349 ACCCATTTGTGAAGCGCGGCCCACTGTGGATTTGAAAACCTGGCATTTATTGATTATG 408
QY 2035 GACCTAGACCCCAACAGAGTGAATGTGGGATGCTTCTGCTA 2077
Db 409 GAATCCGCTCTCAATAGGAGTGAAGATGGGATGCTATTGCTA 451

RESULT 5

US-09-206-695-1
Sequence 1, Application US/09206695
Patent No. 6210905
GENERAL INFORMATION:
APPLICANT: Lee, Tae Ho
APPLICANT: Wisniewski, Hans Georg
APPLICANT: Vilcek, Jan
TITLE OF INVENTION: Cytokine-Induced Protein, TSG-6, DNA Coding
TITLE OF INVENTION: Therefor and Uses Thereof
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street, N.W., Suite 300

```

Therefor and Uses Thereof

NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
ZIP: 20004

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/799,118
FILING DATE: 06-Mar-2001
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/242,097
FILING DATE: 13-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: LEE26/VILCEK=1B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-628-5197
TELEFAX: 212-737-3528

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1414 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
CELL TYPE: Fibroblast
CELL LINE: FS-4

FEATURE:
NAME/KEY: CDS
LOCATION: 69..899
OTHER INFORMATION:
SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-09-799-118-1

Query Match 2.5%; Score 81.4; DB 4; Length
Best Local Similarity 55.5%; Pred. No. 1.3e-13;
Matches 157; Conservative 0; Mismatches 126; Indel

1795 CTGTGGGGTTCATCTACGCTCCCACTGGGCCGAGTATAAGCTGCT
169 CAGCGGTGTGTACACAGAGAAGCAGCGTCTGGCAAAATACAAAGCT
1855 CCAGAGGCGCTGTGGCCAAACCAAGCTCGACCATGGCAACTCAAA
229 CTAAGCGCGTGTGTGAATTTGAAGCGGCCATCTCGCAACTTACAA
1915 CCCAGAGGCCAAGTAGTACCACTGTGCTCAGCAGCGCTGGCTGGAGAC
289 CCAGAAAAATTTGGATTTTCATGCTGTGCTGCTGCGATGGATCGCTAAAG
1975 ACCCCACAGCCTTGCCTCCAGAGACTGTGCTCTGGTGTGGTGGG
349 ACCCCATTGTGAAGCCAGGCGGCCAACTGTGGAATTTGGAAAACTGG
2035 GACCTAGACCCCAACAAGAGTAGTAAATGTGGGATGCTTCTTGCTA 408
GAATCCGCTCAATAGGAGTGAAGATCGGATGCTATTGCTA 45

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CITY: Washington
 STATE: D.C.
 ZIP: 20004
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/206,695
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/242,097
 FILING DATE: 13-MAY-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: BROWDY, Roger L.
 REGISTRATION NUMBER: 25,618
 REFERENCE/DOCKET NUMBER: LEE26/VILCEK-1B
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-628-5197
 TELEFAX: 212-737-3528
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1414 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 ORIGINAL SOURCE:
 ORGANISM: Homo sapiens
 CELL TYPE: Fibroblast
 CELL LINE: FS-4
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 69..899
 OTHER INFORMATION:
 US-09-206-695-1
 Query Match 2.5%; Score 81.4; DB 3; Length 1414;
 Best Local Similarity 55.5%; Pred. No. 1.3e-13;
 Matches 157; Conservative 0; Mismatches 126; Indels 0; Gaps 0;
 QY 1795 CTGTTGGGGTGTTCATCTACGCTCCCACTGGCCAGTAGTAAAGCTTGACCTTTGACAAAG 1854
 Db 169 CAGCCGGGTGTGTACCAAGAGACACGGTCTGTGGCAATACAAAGCTCACCTACGCAGAG 228
 QY 1855 CCAGAGAGGCCCTGTGCCAACGAGCTGCCACCATGGCAACCTACAAACCCAGCTCTCCCTATG 1914
 Db 229 CTAAGCGGTGTGTGAAATTTGAAGCGGCCCATCTCGCAACTTACAAGCAGCTAGAGGCAG 288
 QY 1915 CCCAGAGGCCCAAGTACCACTGTGTCTAGCAGGCTGGCTGGAGACCGGGCGGTTGCCCT 1974
 Db 289 CCAGAAAAATTGGAATTTTCATGTCTGTGCTGTGGATGGCTAAGGGCAGAGTTTGGAT 348
 QY 1975 ACCCCACAGCCCTTCGCCTCCCAAGCTGTGGGCTCTCGTGTGGTTGGATAGTGGACTATG 2034
 Db 349 ACCCCATTGTGAAGCCAGGGGCCCACTGTGGAATTTGAAAACTGGCATTATTGATTATG 408
 QY 2035 GACCTAGACCCCAACAGAGTGAATCTGGGATGCTCTCTGCTA 2077
 Db 409 GAATCCGTCTCAATAGAGTGAAGATGGATGCCTATTGCTA 451

RESULT 7
US-09-484-970B-63
; Sequence 63, Application US/09484970B

Patent No. 6426186
GENERAL INFORMATION:
APPLICANT: Jones, Karen A.
APPLICANT: Volkmut, Wayne
APPLICANT: Walker, Michael G.
TITLE OF INVENTION: BONE REMODELING GENES
FILE REFERENCE: PB-0014 US
CURRENT APPLICATION NUMBER: US/09/484,970B
CURRENT FILING DATE: 2000-01-18
NUMBER OF SEQ ID NOS: 172
SOFTWARE: PERL Program
SEQ ID NO 63
LENGTH: 1734
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc.feature
OTHER INFORMATION: Incyte ID No. 6426186 201752.1
LOCATION: 1444, 1455, 1457, 1461, 1463, 1465, 1467, 1497, 1500, 1506, 1521, 1534-
OTHER INFORMATION: a, t, c, g, or other
US-09-484-970B-63

Query Match 2.2%; Score 72; DB 4; Length 1734;
Best Local Similarity 55.6%; Pred. No. 9.2e-11;
Matches 158; Conservative 0; Mismatches 125; Indels 1; Gaps 1;

QY 1795 CTGTTGGGGTTCATCTACGCTCCCACTGGCCAGTATAGCTGACCTTTGACAAG 1854
DB 169 CAGCGGTGTGTACACAGAGACGCGTCTGGCAATACAACTCACCTACGAGAAG 228
QY 1855 CCAGAGAGCGCTGTCCCAACGAGCTGCACCTACGACCTACCAAGCTCTCTATG 1914
DB 229 CTAGGCGGTGTGTAAATTGAAGCGCGCCACTCTCCCACTTACCAAGCAGCTAGAGGCG 288
QY 1915 CCCAGAGCGCAAGTACCACCTGTCTCAGCAGGCTGGCTGAGACCGCGGGTTCCT 1974
DB 289 CCAGAAAATTGGATTTCATCTCTGTCTGTCTGTGATGATGCTAAGGCGAGATTGGAT 348
QY 1975 ACCCCACAG-CCTTCGCTCCCAAGTGTGGCTCTGGTGTGGTGGATAGTGGACTAT 2033
DB 349 ACCCCATTGTGAAGCGAGCGGCCCACTGTGGATTGGAAAACTGGCATATTGATTAT 408
QY 2034 GGACCTAGACCCCAAGAGTGAATGTGGGATGCTTCTGCTA 2077
DB 409 GGAATCCCTCAATAGGAGTGAAGATGGGATGCTTATGCTA 452

RESULT 8

US-09-907-794A-212
Sequence 212, Application US/09907794A
Patent No. 6635468
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnovers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerriksen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kijavini, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/907,794A
CURRENT FILING DATE: 2001-07-17
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 212
LENGTH: 1985
TYPE: DNA
ORGANISM: Homo sapiens
US-09-907-794A-212

Query Match 1.8%; Score 58.6; DB 4; Length 1985;
Best Local Similarity 55.0%; Pred. No. 9.6e-07;
Matches 115; Conservative 0; Mismatches 94; Indels 0; Gaps 0;

QY 1797 GTTGGGGTGTTCATCTACGCTCCCACTGGCCAGTATAGCTGACCTTTGACAAGCC 1856
DB 593 GGTGTGTCTTCTCTCTTACCACTCCCAACCGGCGCTACCACTTCACTCCAGAGGCG 652
QY 1857 AGAGAGCGCTGTGCCAAGAGCTGCCAGCATGCAACCTTACACAGCTCTCTATGCC 1916
DB 653 CAGCAGGTCTGTGCAGAGCAGGCTGCGGTGGTGGCTCTCTTTGAGCAGCTCTCCGGGCC 712
QY 1917 CAGAAGGCCAAGTACCACTGTGCTCAGCAGGCTGGCTGGAGACCGGGCGGTTGCCCTAC 1976
DB 713 TGGAGAGAGGCGCTGGACTGTGTGCAACCGGCGCTGGCTGAGATGTACGGTGCAGTAC 772
QY 1977 CCCAGACCTTTCGCTCTCCCAAGAACTGTGG 2005
DB 773 CCCATCATGTTGCCCGCGGAGCCCTGCGG 801

RESULT 9

US-09-905-125A-212									
; Sequence 212, Application US/09905125A									
; Patent No. 6664376									
; GENERAL INFORMATION:									
; APPLICANT: Genentech, Inc.									
; APPLICANT: Ashkenazi, Avi									
; APPLICANT: Botstein, David									
; APPLICANT: Desnoyers, Luc									
; APPLICANT: Eaton, Dan L.									
; APPLICANT: Ferrara, Napoleone									
; APPLICANT: Filvaroff, Ellen									
; APPLICANT: Fong, Sherman									
; APPLICANT: Gao, Wei-Qiang									
; APPLICANT: Gerber, Hanspeter									
; APPLICANT: Gerritsen, Mary E.									
; APPLICANT: Goddard, A.									
; APPLICANT: Godowski, Paul J.									
; APPLICANT: Grimaldi, Christopher J.									
; APPLICANT: Gurney, Austin L.									
; APPLICANT: Hillan, Kenneth, J.									
; APPLICANT: Kijavin, Ivar J.									
; APPLICANT: Mather, Jennie P.									
; APPLICANT: Pan, James									
; APPLICANT: Paoni, Nicholas F.									
; APPLICANT: Roy, Margaret Ann									
; APPLICANT: Stewart, Timothy A.									
; APPLICANT: Tumas, Daniel									
; APPLICANT: Williams, P. Mickey									
; APPLICANT: Wood, William, I.									
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic									
; TITLE OF INVENTION: Acids Encoding the Same									
; FILE REFERENCE: 10466-14									
; CURRENT APPLICATION NUMBER: US/09/905,125A									
; CURRENT FILING DATE: 2001-07-12									
; PRIOR APPLICATION NUMBER: PCT/US00/04414									
; PRIOR FILING DATE: 2000-02-22									
; PRIOR APPLICATION NUMBER: US 60/143,048									
; PRIOR FILING DATE: 1999-07-07									
; PRIOR APPLICATION NUMBER: US 60/145,698									
; PRIOR FILING DATE: 1999-07-26									
; PRIOR APPLICATION NUMBER: US 60/146,222									
; PRIOR FILING DATE: 1999-07-28									
; PRIOR APPLICATION NUMBER: PCT/US99/20594									
; PRIOR FILING DATE: 1999-09-08									
; PRIOR APPLICATION NUMBER: PCT/US99/20944									
; PRIOR FILING DATE: 1999-09-13									
; PRIOR APPLICATION NUMBER: PCT/US99/21090									
; PRIOR FILING DATE: 1999-09-15									
; PRIOR APPLICATION NUMBER: PCT/US99/21547									
; PRIOR FILING DATE: 1999-09-15									
; PRIOR APPLICATION NUMBER: PCT/US99/23089									
; PRIOR FILING DATE: 1999-10-05									
; PRIOR APPLICATION NUMBER: PCT/US99/28214									
; PRIOR FILING DATE: 1999-11-29									
; PRIOR APPLICATION NUMBER: PCT/US99/28313									
; PRIOR FILING DATE: 1999-11-30									
; PRIOR APPLICATION NUMBER: PCT/US99/28564									
; PRIOR FILING DATE: 1999-12-02									
; PRIOR APPLICATION NUMBER: PCT/US99/28565									
; PRIOR FILING DATE: 1999-12-02									
; PRIOR APPLICATION NUMBER: PCT/US99/30095									
; PRIOR FILING DATE: 1999-12-16									
; PRIOR APPLICATION NUMBER: PCT/US99/30911									
; PRIOR FILING DATE: 1999-12-20									
; PRIOR APPLICATION NUMBER: PCT/US99/30999									
; PRIOR FILING DATE: 1999-12-20									
; PRIOR APPLICATION NUMBER: PCT/US00/00219									
; PRIOR FILING DATE: 2000-01-05									
; NUMBER OF SEQ ID NOS: 423									
; SEQ ID NO 212									
; LENGTH: 1985									
; TYPE: DNA									
; ORGANISM: Homo sapiens									
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; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-15
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 212
; LENGTH: 1985
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-902-775A-212

Query Match 1.8%; Score 58.6; DB 4; Length 1985;
Best Local Similarity 55.0%; Pred. No. 9.6e-07;
Matches 115; Conservative 0; Mismatches 94; Indels 0; Gaps 0;
QY 1797 GTTGGGGTGTCCATCTACGCTCCCTCCCTGCGCCAGTATAGCTGACCTTTGACAAAGCC 1856
Db 593 GGTGTGCTTCTTCTTACAGTCCCTCCCTCCCTGCGCCAGTATAGCTGACCTTTGACAAAGCC 652
QY 1857 AGAGAGGCTGTGCAAGCAAGCTGCGACCATGCGCAACCTACCAACCACTCTCTATGCC 1916
Db 653 CAGCAGGTCTGTGAGAGCAGCTGCGGTGTGCGCTCTTTGACGAGCTTTCCGGGCC 712
QY 1917 CAGAGGCAAGTACCACTGTGTGAGAGGCTGCGGTGTGAGAGCGGCGCGGTGCGCTTAC 1976
Db 713 TGGAGAGGAGGCGCTGGAAGTGTGCAACGCGGCTGCGGTGCGAGTGTACGGTGCAGTAC 772
QY 1977 CCACAGCCTTCCCTCCCTCCCTGCGCCAGTGTGG 2005
Db 773 CCATCATGTGCGCGCAGCCCTGCGG 801

RESULT 11
US-08-232-463-14/c
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: pTZgpt-F1s
US-08-232-463-14

Query Match 1.7%; Score 54.2; DB 1; Length 7218;
Best Local Similarity 3.6%; Pred. No. 4.6e-05;
Matches 14; Conservative 221; Mismatches 154; Indels 0; Gaps 0;
QY 1392 AAGGAGAACACAGCTGTGAGTGAACCTGATTATGAAGTGAAGGAGGATCACATGCACA 1451
Db 1432 RRR 1373
QY 1452 GTTGTGATTCTTCAACACAGGACAAAGGGGGCTGTGCAAGGTGCGCAGATGCTCCAG 1511
Db 1372 RRR 1313
QY 1512 AAGGCGCAGAGTCTCTGAGTGCAGAGGATACAAAGGGGACGGGACAGCTGC 1571
Db 1312 RRR 1253
QY 1572 ACAGAGATAGACCCCTGTGAGCAGCGCTTAACGAGGGGTGACGAGCAGCCACCTGT 1631
Db 1252 RRR 1193
QY 1632 AAGATGACAGCGCGGCAAGCAAGTGTGAGTGAAGTCACTATGTCGAGATGGG 1691
Db 1192 RRR 1133
QY 1692 CTGAACCTGAGCGGAGCAGCTGCCCATTCGACCGCTTACAGGACAATGGGACGTC 1751
Db 1132 RRR 1073
QY 1752 CATGACAGCGCAAAATGTGCGACCTCCA 1780
Db 1072 RRRRRATCGCAAGCTCCCTCGACCTGCA 1044

RESULT 12
US-08-001-078A-2
; Sequence 2, Application US/08001078A
; Patent No. 5872094
; GENERAL INFORMATION:
; APPLICANT: Goetinck, Paul F.
; APPLICANT: Tondravi, M., Mehrdad
; APPLICANT: Binette, Francois
; TITLE OF INVENTION: METHODS FOR PROMOTING CARTILAGE MATRIX
; TITLE OF INVENTION: FORMATION
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 STATE STREET, Suite 510
; CITY: BOSTON
; STATE: Massachusetts
; COUNTRY: USA

ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/001,078A
FILING DATE: 06-JAN-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Myers, Paul L.
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: MGP-008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1400 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-001-078A-2

Query Match 1.7%; Score 53.8; DB 2; Length 1400;

Best Local Similarity 53.6%; Pred. No. 2e-05; Mismatches 0; Indels 0; Gaps 0;

Matches 112; Conservative 0; Mismatches 97; Indels 0; Gaps 0;

QY 1797 GTTGGGGTGTCCATCTACGCTCCCACTGGGCCAGTATAGCTGACCTTTGACAAAGCC 1856

DB 706 GGTGTGGTATTCCTTACTTCCACGACTGGGGCGCTACAATCTCAATTTTCACGAGGG 765

QY 1857 AGAGAGGCGCTGTGCCAAGCAAGCTGCGACCTGGCCAGTATAGCTGACCTTTGACAAAGCC 1916

DB 766 CAGCAGGCGCTGTCTGGACCAAGATGCTGTGATCGCTCTTCCGACCAAGCTGACGAGCC 825

QY 1917 CAGAGGCGCTGTGCCAAGCAAGCTGCGACCTGGCCAGTATAGCTGACCTTTGACAAAGCC 1976

DB 826 TGGCGGGGGCGCTGGAGTGGTGCAATGCCGCTGGCTCAGTGATGGCTCTCTGTGCAATCT 885

QY 1977 CCCACAGCCTTCGCTCCCAAGCAAGCTGCGACCTGGCCAGTATAGCTGACCTTTGACAAAGCC 2005

DB 886 CCCATCAAAAGCCAGAGAGCCCTGTGG 914

RESULT 13

US-08-463-218-2

Sequence 2, Application US/08463218

Patent No. 5986052

GENERAL INFORMATION:

APPLICANT: Goetinck, Paul F.

APPLICANT: Tondravi, Mehrdad

APPLICANT: Binette, Francois

TITLE OF INVENTION: METHODS FOR PROMOTING CARTILAGE MATRIX

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSEE: LAHIVE & COCKFIELD

STREET: 60 STATE STREET, Suite 510

CITY: BOSTON

STATE: Massachusetts

COUNTRY: USA

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/463,218

FILING DATE: 05-JUNE-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/001,078
FILING DATE: 06-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Myers, Paul L.
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: MGP-008DV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1400 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-463-218-2

Query Match 1.7%; Score 53.8; DB 2; Length 1400;

Best Local Similarity 53.6%; Pred. No. 2e-05;

Matches 112; Conservative 0; Mismatches 97; Indels 0; Gaps 0;

QY 1797 GTTGGGGTGTCCATCTACGCTCCCACTGGGCCAGTATAGCTGACCTTTGACAAAGCC 1856

DB 706 GGTGTGGTATTCCTTACTTCCACGACTGGGGCGCTACAATCTCAATTTTCACGAGGG 765

QY 1857 AGAGAGGCGCTGTGCCAAGCAAGCTGCGACCTGGCCAGTATAGCTGACCTTTGACAAAGCC 1916

DB 766 CAGCAGGCGCTGTCTGGACCAAGATGCTGTGATCGCTCTTCCGACCAAGCTGACGAGCC 825

QY 1917 CAGAGGCGCTGTGCCAAGCAAGCTGCGACCTGGCCAGTATAGCTGACCTTTGACAAAGCC 1976

DB 826 TGGCGGGGGCGCTGGAGTGGTGCAATGCCGCTGGCTCAGTGATGGCTCTCTGTGCAATCT 885

QY 1977 CCCACAGCCTTCGCTCCCAAGCAAGCTGCGACCTGGCCAGTATAGCTGACCTTTGACAAAGCC 2005

DB 886 CCCATCAAAAGCCAGAGAGCCCTGTGG 914

RESULT 14

PCT-US94-00253-2

Sequence 2, Application PC/TUS9400253

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: METHODS FOR PROMOTING CARTILAGE MATRIX

TITLE OF INVENTION: FORMATION

NUMBER OF SEQUENCES: 2

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII (text)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US94/00253

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/001,078

FILING DATE: 06-JAN-1993

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 1400 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

PCT-US94-00253-2

Query Match

Best Local Similarity 1.7%; Score 53.8; DB 5; Length 1400;

Matches 112; Conservative 0; Mismatches 97; Indels 0; Gaps 0;

QY 1797 GTTGGGGTGTCCATCTACGCTCCCACTGGGCCAGTATAGCTGACCTTTGACAAAGCC 1856

DB 706 GGTGTGGTATTCCTTACTTCCACGACTGGGGCGCTACAATCTCAATTTTCACGAGGG 765

QY 1857 AGAGAGGCGCTGTGCCAAGCAAGCTGCGACCTGGCCAGTATAGCTGACCTTTGACAAAGCC 1916

Db 766 CAGCAGGCTGTCTGAGCAGATGCTGTATCGCCTCTTCGACCACTGTACGACGCC 825
Qy 1917 CAGAAGGCAAGTACCACTGTCTGCTCAGCAGGCTGGCTGGAGACCGGGCGGTTGCCCTAC 1976
Db 826 TGGCGGGCGGCTGCACTGTGTGCAATGCCGGCTGGCTCAGTGATGGCTCTGTGCAATCT 885
Qy 1977 CCCACAGCTTCGGCTCCCAAGACTGTGG 2005
Db 886 CCCATCAACAAGCCAGAGAGCCCTGTGG 914

RESULT 15

US-08-232-463-14
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFELINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: ptzgt-F1s
US-08-232-463-14

Query Match 1.6%; Score 52.8; DB 1; Length 7218;
Best Local Similarity 2.7%; Pred. No. 0.00012;
Matches 9; Conservative 198; Mismatches 126; Indels 0; Gaps 0;
Qy 2870 TGGACGGGAGATGCCACATCACTCACTGCCACCTGGGCGCATCACTGTAATTCAG 2929
Db 1050 TCGAGGAGCTTGGATTT 1109
Qy 2930 CACCAGTTGCTTTTAGAAGCTAAAGTCTTTAAGCACTCAGAAAGCCATACCTCATCTC 2989
Db 1110 YY 1169

Qy 2990 TCTGGCTGAATCTGGGGGTGTGTTCTGTGGGTGAGAGATGTGTGCTGCCCCACCCAGTA 3049
Db 1170 YY 1229
Qy 3050 CAGCTTCTCTCTGACCCCTTTGGCTCTTCTCTCTTGTACTCTTCACTGGCAGCTGCT 3109
Db 1230 YY 1289
Qy 3110 CCATTCTGCCCTACATGATGGTAACCTGATCTTCTTCCCTGTTAGATTGTAGACCTC 3169
Db 1290 YY 1349
Qy 3170 CNTCTTGTATCCAGCCCTTAGCCAGTGCCT 3202
Db 1350 YY 1382

Search completed: June 21, 2004, 16:27:07
Job time : 222 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 21, 2004, 10:16:51 ; Search time 7854 Seconds
(without alignments)

12395.048 Million cell updates/sec

Title: US-10-028-248A-210

Perfect score: 3260

Sequence: 1 ggcacgacgagcttccc.....aaaaaaaaaaaaaaaaaaaa 3260

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_estl:*
10: gb_est2:*
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14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	ID	Description
1	1852.6	56.8	3085	11 AK034522
C 2	735.8	22.6	741	14 CA449310
C 3	591	18.1	605	14 CA433190
4	510	15.6	524	13 BX101101
				EX101101 BX101101

5	486	14.9	562	12	BG220572
C 6	472	14.5	481	9	AI081595
C 7	441.4	13.5	455	9	AI248408
C 8	418.4	12.8	421	9	AI131339
C 9	413.6	12.7	664	10	BB626584
C 10	404.2	12.4	488	14	R92610
C 11	401.4	12.3	422	9	AA968560
C 12	381	11.7	448	14	H49176
C 13	378.2	11.6	484	9	AA010567
C 14	370.4	11.4	3025	11	BC049247
C 15	358.4	11.0	396	14	H31274
C 16	355	10.9	819	13	BX171115
C 17	333	10.2	334	9	AI084842
C 18	332.4	10.2	445	14	H90364
C 19	329.8	10.1	459	14	T47504
C 20	329	10.1	453	14	H49088
C 21	328.8	10.1	545	28	AQ278586
C 22	326	10.0	331	14	R97435
C 23	323	9.9	324	9	AA704436
C 24	322.6	9.9	414	14	H70480
C 25	322.2	9.9	460	14	R97483
C 26	314	9.6	325	9	AA257161
C 27	313.2	9.6	1155	12	EM913585
C 28	305.4	9.4	394	9	AA004325
C 29	301	9.2	302	9	AA257068
C 30	300.8	9.2	2368	11	BC019712
C 31	286.4	8.8	694	14	CA376384
C 32	283.6	8.7	683	12	BJ523552
C 33	273.2	8.4	348	14	R91674
C 34	270.8	8.3	328	14	R91675
C 35	269.8	8.3	793	12	B1832486
C 36	247.8	7.6	385	10	BB842118
C 37	240	7.4	601	14	CB513007
C 38	216.4	6.6	228	14	T47505
C 39	208.4	6.4	500	9	AA821602
C 40	208	6.4	722	13	BX739778
C 41	206.8	6.3	462	10	BE556181
C 42	203	6.2	809	9	AU080852
C 43	199	6.1	928	12	BI906024
C 44	194.6	6.0	660	13	BX265613
C 45	192	5.9	612	13	BX265614

ALIGNMENTS

RESULT 1

AK034522

LOCUS

DEFINITION

AK034522

ACCESION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

AK034522 3085 bp mRNA linear HTC 18-SEP-2003
Mus musculus adult male diencephalon cDNA, RIKEN full-length
enriched library, clone:9330210123 product:similar to CD44-LIKE
PRECUSOR FELL [Homo sapiens], full insert sequence.

AK034522 GI:26330004

HTC; CAP trapper.

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,

Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

Normalization and subtraction of cap-trapper-selected cDNAs to

prepare full-length cDNA libraries for rapid discovery of new genes

Genome Res. 10 (10), 1617-1630 (2000)

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Db 664 CTGCTAATGGATCCTACCGAAGGTGGCCGATGTGACACTTTTACTACCTTCAATATTCGG 723
QY 906 GGGGAGTGTGGAGCTGTGTCAATACTCCAGCTGCCAAGGTGGAGTAACCAAAAGGAT 965
Db 724 GGGGAAATGTGGGAGCTGTGTTCCTCACTCCAGATGCCACTACAGAGCAAAACAAAGGAT 783
QY 966 GTGAAGCAGAAAGTGTCTCTACAACTG---CCCTTCAGAGAGAACTTGGAGGCTGCCGG 1022
Db 784 GTGAGGAAGAAGTGTATCTACAAACCGGTACCTTTTCAGAGGGATGTGGAAGGCTGTCA 843
QY 1023 GAGCGGTGCAGCTGTGTGATACAGATCCCGAGGTGTCTGCAAGGGCTACTTCGGGGCAGAC 1082
Db 844 AACCTGTGCACCTGTGTGTTCATGTCCGCGGTGTGAGTGTGATCTTTCATGACAGAC 903
QY 1083 TGTGAGGCTGTGCTGTGAGGACAGATGCCCGTGTAAATAACCGGGGTGTCTGCCCTTGAT 1142
Db 904 TGTGAGGCTGTGCTGTGAGGACAGACACACCGTGTAAACCGGGCATGTGTATGAT 963
QY 1143 CAGTACTCGGCCACCGAGAGTGTAAATGCAACACCGGCTTCAATGGGACGGGTGTGAG 1202
Db 964 CAGTACAAACCCACAGGACAGTGCCTGTATCTGTTTCAACGGGACAGCTGTGAG 1023
QY 1203 ATGTGCTGGCGGGAGATTCGGGCTGTGTTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGT 1262
Db 1024 CTCTGCTGTGCTGGGAGATTTGGTCTGACTGTCAACCTGTGCTGTGCTGTGCTGTGCTGT 1083
QY 1263 CAGTGCAGATGATGGATCAGCGGCTCCGGGAGTGCCTGTGTGAAACCGGGGTGGACAGGC 1322
Db 1084 CAGTGTGACGAGGGGATCACAGGCTCCGGGAGTGCCTCTGTGAAGCAGGGGTGGACAGGC 1143
QY 1323 CCCTGCTGTGACACTCAGCGAGTTTGGCTGTGAGTGTGACGCTTACCTGTGCTGTGCTGT 1382
Db 1144 GCCTCTGTGATGCTCCACAGTGTGTGATCCAGTGTGATACCTGTGCTGTGCTGTGCTGT 1203
QY 1383 GCCACCTGTAAGGAGAAACAACGCTGTGAGTGTAACTGTGATTAAGAGTGAACGGAATC 1442
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Db 1624 GTATTTCACCTTACGCTCCCACTGGGCGAGTACAACTGACATTTGACAAAGCCAAAGAG 1683
QY 1863 GCCTGTGCAACGAGCTGGACCATGTGCAACCTTACACAGCTCTCTATGCCCCAGAG 1922
Db 1684 GCCTGTGCAACGAGCTGGATTCATAGCACCTTACAAACAGCTCTCTATGCCCCAGAG 1743
QY 1923 GCCAAGTACCACTGTGTGACAGAGGTGGCTGGAGACCGGGGGTGTGCTACCCCA 1982
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QY 1983 GCCTCGGCTCCACAGAACTGTGGCTCTGGTGTGGTGTGGATAGTGAAGTATGACCTAGA 2042
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QY 2043 CCCAAACAGAGTGAATGTGGGATGTCTTCTGTCTATCGGATGAAAGATGTGAAGTGCACC 2102
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QY 2103 TGCAAGGTGGCTATGTGGGAGATGGCTTCTCATGCTGAGTGGGAACTGCTGAGGTCTG 2162
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QY 2163 ATGTCTTCTCCCTCACTCACAACTTCTGACGGAAGTGTCTGCTATTTCCAAACAGCTCA 2222
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QY 2343 CACCTGCGCAATGTGAGCATGTTTTTCTCAATGACCTTGTCAATGGCACCACTCGCAA 2402
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QY 2403 ACAGGGTGGGAAGCAGCTGCTCATCTGCTGAGCAGGACCCACTCCAAACGAGCAG 2462
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QY 2463 ACCAGGTTGTGTGATGAAGAGCAATCTGAGTGGGAGCATCTTGTGCTCCAAATGGGATC 2522
Db 2278 GCGAGGTTGTGTGATGAAGAGCCATCTGCGTGGGACATCATTTGCTCTTAAAGGGGTT 2337
QY 2523 ATTCATGCTCAATTTCCAGGCTTTTAAAGCACCCCTGCCCCCGTGACCTTGACCCACACT 2582
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QY 2583 GGCTTGGAGCAGGATCTCTTTGCCATCATCTCTGTGATCTGGGCTGTGCTTGGCT 2642
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QY 2643 GCTTACTCTTACTTTTCGATTAACCGGAGAACATCGGCTTCCAGCATTTTGTGAGTCGAA 2702
Db 2458 GCCTACTCTTACTTCCGGCTTAAACAGAGAACAACTGCTTCCGGCGTTTTGTGAGTCAGAA 2517
QY 2703 GAGGACATTAATGTGAGCTCTTTGGCAAGCAGGAGCTGTAGAAATATCTCGAACCCCTTG 2762
Db 2518 GATGACATGATGCTTTGGCTTTTGGCAAGCAGCAGCCTGTAGAGTATCACAAACCTTTG 2577
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QY 2823 GAACGGCAGCTTGAGGCGCAATGACCCCTTGAGGACACTGTGAGGCGCTTGACGGGAGATG 2882
Db 2638 GAACGGGAGCTTGAGAACAGTGAACCTCTTGGGCACTG---AGGTCTGTATGTGAGAAG 2694
QY 2883 CCAGCCATCACTCACTGCCACCTGGGCCATCA-----ACTGTGAATTTCTCA 2928
Db 2695 CCAGCCAAACAGCCACAGCCACGTGAGCCCTGAGCCATCACGGTTACACGGTGTCTCCCT 2754
QY 2929 GCACAGTTGCCCTTTAG----GAACGTAAAGTCTTTTAAAGTATGATAAATCTCAGAGCCATCACTCA 2985
Db 2755 GCTCCAGCTGTCACTTGGATCATTTGTTTTTAAAGTATGATAAATCTCAGAGCCATCACTCA 2814
QY 2986 TCTCTCTGGCTGTGATCTGGGGGTTGTTTCTGTGGTGTGAGAGATGTGTGCTGTGCCACCC 3045
Db 2815 CCCCTCTGGTGTGCTGGGGTTGTGCTCATGGGTAAAGGGACATGTTTTTCCAGGACACAG 2874

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@uiowa.edu
The following repetitive elements were found in this cDNA
sequence: 22-83, >LINE2 (matched complement)
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES

source
1..605
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-CO0-ark-g-11-0-UI"
/tissue_type="mixed"
/dev_stage="mixed"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI CGAP Sub9"
/note="Vector: pT7T3-Pac (Pharmacia) with a modified
polylinker; Site 1: EcoR I; Site 2: Not I; tissues:
Cholonic mucosa with Crohns disease, Cholonic mucosa with
ulcerative colitis, Fetal thymus, Cervix, Cervical
adenosquamous carcinoma, Ligament cells, Prostate
carcinoma, Bladder carcinoma, Brain oligodendrocyte ;
NCI CGAP Sub9 is a subtraced cDNA library constructed
according to Bonaldo, Lennon and Soares, Genome Research,
6:791-806, 1996. First strand cDNA synthesis was primed
with an oligo-dT primer containing a Not I site. Double
stranded cDNA was ligated to an EcoR I adaptor, digested
with Not I, and cloned directionally into pT7T3-Pac
vector. The oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tags for this library are CGTC, AACG, GGGCC,
GGAAG, TAGC, TAAGC, ATGGC, AGACA, ATCAC. For additional
information, contact: Bento Soares, bento-soares@uiowa.edu
TAG TISSUE=colonic mucosa with Crohns disease
TAG_LIB=UI-H-CO0
TAG_SEQ=CGTC"

ORIGIN

Query Match 18.1%; Score 591; DB 14; Length 605;
Best Local Similarity 99.3%; Pred. No. 6.3e-98;
Matches 602; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
QY 2653 ACTTTCGATTAACCGGAGAACATCGCGCTCCAGCATTTGAGTCGGAAGAGACATTA 2712
DB 605 ACTTTCGATTAACCGGAGAACATCGCGCTCCAGCATTTGAGTCGGAAGAGACATTA 546
QY 2713 ATGTTGACAGCTCTTGGCAAGCAGCAGCTGAGATATCTCGAACCCCTTGATGAGACA 2772
DB 545 ATGTTGACAGCTCTTGGCAAGCAGCAGCTGAGATATCTCGAACCCCTTGATGAGACA 486
QY 2773 CAACCTCAGCTCCCGCAGACCTTCTACGACCCCTTCACGAGCTCTCGAAGAACGGCAGC 2832
DB 485 CAACCTCAGCTCCCGCAGACCTTCTACGACCCCTTCACGAGCTCTCGAAGAACGGCAGC 426
QY 2833 TTGAGGGCAATGACCCCTTGAGGACACATGTCGAGGGCTGAGCGGAGATGCCAGCATCA 2892
DB 425 TTGAGGGCAATGACCCCTTGAGGACACATGTCGAGGGCTGAGCGGAGATGCCAGCATCA 366
QY 2893 CTCACTGCCACTGGGCCATCACTGTAATTTCTCAGCAGCAGTGCCTTTTAGGACGT 2952
DB 365 CTCACTGCCACTGGGCCATCACTGTAATTTCTCAGCAGCAGTGCCTTTTAGGACGT 306
QY 2953 AAAGTCTCTTAAAGCACTCAGAACCCATACCTCATCTCTCGGCTGATCTGGGGTGTGTT 3012
DB 305 AAAGTCTCTTAAAGCACTCAGAACCCATACCTCATCTCTCGGCTGATCTGGGGTGTGTT 246
QY 3013 CTGTGGGTGAGAGATGTTGCTGTGCCACCCAGTACAGCTTCTCTCTGACCCCTTG 3072
DB 245 CTGTGGGTGAGAGATGTTGCTGTGCCACCCAGTACAGCTTCTCTCTGACCCCTTG 186
QY 3073 GCTCTCTCTCTTGTACTCTTCAGCTGGCACCTGCTCTCACTCTGCCCCATGATGGGT 3132

DB 185 GCTCTCTCTCTTGTACTCTTCAGCTGGCACCTGCTCCATCTGCCCCATGATGGGT 126
QY 3133 AACTGTGATCTTCTTCCCTGTAGATTGTAAGCCTCCTTCTGATCCAGCCCTAG 3192
DB 125 AACTGTGA-CTTCTTCCCTGTAGATTGTAAGCCTCCTTCTGATCCAGCCCTAG 67
QY 3193 CCCAGTGCTGACACAGGAACCTGTGCACAATAAAGGTTTATGGAACAGAAAAA 3252
DB 66 CCCAGTGCTGACACAGGAACCTGTGCACAATAAAGGTTTATGGAACAGAAAAA 7
QY 3253 AAAAAA 3258
DB 6 AAAAAA 1

RESULT 4

LOCUS BX101101 524 bp mRNA linear EST 06-FEB-2003
DEFINITION BX101101 Soares fetal liver spleen INFLS Homo sapiens cDNA clone
IMAGE998013518 ; IMAGE:241380, mRNA sequence.
ACCESSION BX101101
VERSION BX101101.1 GI:27831018
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 524)
AUTHORS Ebert,J., Heil,O., Hennig,S., Neubert,P., Partsch,E., Peters,M.,
Radelof,U., Schneider,D. and Korn,B.
HUMAN UNIGENES - RZPD3
UNPUBLISHED (2003)
CONTACT: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
RZPD; IMAGE998013518.
RZPDLIB; I.M.A.G.E. cDNA Clone Collection;
http://www.rzpd.de/CloneCards/cgi-
bin/showlib.pl.cgi/response?libNo=972 Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 101
Fax: +49 30 32639 111
www.rzpd.de
This clone is available royalty-free from RZPD;
contact RZPD (clone@rzpd.de) for further information. Seq primer:
M13r, Primer sequence: TTTCACACAGGAACAGCTATGAC.
FEATURES
source
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE998013518 ; IMAGE:241380"
/sex="male"
/dev_stage="20 week-post conception fetus"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares fetal liver spleen INFLS"
/note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
with a modified polylinker; Site 1: Pac I; Site 2: Eco RI;
1st strand cDNA was primed with a Pac I - oligo(dT) primer
[5', AACTGGAAGAAATTAATAAGATCTTTTTTTTTTTT 3'],
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Pac I and cloned into the Pac I
and Eco RI sites of the modified pT7T3 vector. Library
went through one round of normalization. Library
constructed by Bento Soares and M.Fatima Bonaldo."

ORIGIN

Query Match 15.6%; Score 510; DB 13; Length 524;
Best Local Similarity 99.2%; Pred. No. 4.3e-83;
Matches 523; Conservative 0; Mismatches 1; Indels 3; Gaps 1;

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/clone_lib="Athersys RAGE Library"
/note="See 'Creation of Genome-wide Protein Expression
Libraries using Random Activation of Gene Expression',
Nature Biotechnology, in press. Note that even though the
cell type indicated is HT1080, since a random activation
method was used, these sequence tags are not necessarily
expressed in HT1080 under normal circumstances."
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ORIGIN

Query Match	14.9%;	Score 486;	DB 12;	Length 562;
Best Local Similarity	94.7%;	Pred. No. 1e-78;		
Matches 534;	Conservative 0;	Mismatches 27;	Indels 3;	Gaps 3;
QY	2690	TTTGTAGTCGGAAGAGGACATTAATCTTGTCAGCTCTTGGCAAGCAGCAGCCTGAGAAATAT	2749	
DB	2	TTGTGTCGGGACTGAGGACATTAATGTTGAGGTCTTACCAAGCAGTAGCCTGAGAAATAT	61	
QY	2750	CTCGAACCCCTTGTATGAGAGCAACAACCTCAGCTCCCCAGAACACCTTCTTACGACCCCTT	2809	
DB	62	CTCGAATCCCTTGTATGAGAGCAACAACCTCAGCTCCCCAGAACACCTTCTTACGACCCCTT	121	
QY	2810	CACGGACTCTGAAAGACGGCAGCTTCAGGGCAATGACCCTTTCAGGACACACTGTGAGGGCC	2869	
DB	122	CACGGACTCTGAAAGAACGGCAGCTTTCAGGGCAATGACCCTTTCAGGACACACTGTGAGGGCC	181	
QY	2870	TGGAACGGGAGATGCCAGCCATCACTCACTGCCACCTGGGCGCATCAACTGTGGAATCTTCAG	2929	
DB	182	TGGAACGGGAGATGCCAGCCATCACTCACTGCCACCTGGGCGCATCAACTGTGGAATCTTCAG	241	
QY	2930	CACAGTTGGCTTTTAGGAACGTAAGTCCCTTTAAGCACTCAGAAGCCATACCTCATCTC	2989	
DB	242	CACAGTTGGCTTTTAGGAACGTAAGTCCCTTTAAGCACTCAGAAGCCATACCTCATCTC	301	
QY	2990	TCGTGGCTGATCTGGGGGTCTCTTCTGTGGGTGAGAGATGTGTCTGTGCCACCCAGTA	3049	
DB	302	TCGTGGCTGATCTGGGGGTCTCTTCTGTGGGTGAGAGATGTGTCTGTGCCACCCAGTA	361	
QY	3050	CAGCTTCCTCCTCTGACCCCTTTGGCTCTTCTCTTTGTACTCTTTCAGCTGGGACCTGCT	3109	
DB	362	CAGCTTCCTCCTCTGACCCCTTTGGCTCTTCTCTTTGTACTCTTTCAGCTGGGACCTGCT	421	
QY	3110	CCATTGCGCCCTACATGATGGGTAACTGTGATCTTCTTCCTCTGTAGATTGTAAAGCCTC	3169	
DB	422	CCATTCTGCCCTACATGATGGGTAACTGTGATC-TTCTTCCCTCTGTAGATTGTAA-CCTT	479	
QY	3170	CNTCTTTGTATCCAGAGCCCTTAGCCCAAGTCGCTTGACACAGGAACCTGTGCACAAATAAGGT	3229	
DB	480	CAGCTTTGTATCCCA-CCCTTAACCCAAATGCCTTGACACAGGACTGTGCACACAAAGG	538	
QY	3230	TTATGGAACAGAAAAAAAAAAAAA	3253	
DB	539	TTATGGAACAGAAAAAAAAAAAAA	562	

RESULT 6

AI081595/c	AI081595	481 bp	linear	EST 28-AUG-1998
LOCUS	ox63h05.s1 Soares_NhMPu_S1	Homo sapiens	cdna	IMAGE:1661049
DEFINITION	3', mRNA sequence.			
ACCESSION	AI081595			
VERSION	AI081595.1			
KEYWORDS	EST.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
REFERENCE	1 (bases 1 to 481)			
AUTHORS	NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap .			
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),			
	Tumor Gene Index			
JOURNAL	Unpublished (1997)			
COMMENT	Contact: Robert Strausberg, Ph.D. Email: ccapbs-t@mail.nih.gov			

2729	Qy	CAAGCAGACGCTGAGAAATCTCGAACCCCTGTGTATGAGAGACACACTCAGCTCCCC	2788
1	Db	CAAGCAGACGCTGAGAAATCTCGAACCCCTGTGTATGAGAGACACACTCAGCTCCCC	60
2789	Qy	AGAACCTTCTACGACGCCCTTTCACGGACTCTGAAGAACGGCAGCTTGAGGGCAATGACCC	2848
61	Db	AGAACCTTCTCT--ACCCCTTACGGACTCTGAAGAACGGCAGCTTGAGGGCAATGACCC	117
2849	Qy	CTTGAGGACACTGTGAGGGGCTGAGCGGAGATGCGAGCCATCATCTCAGTCGCCACCTGGG	2908
118	Db	CTTGAGGACACTGTGAGGGGCTGAGCGGAGATGCGAGCCATCATCTCAGTCGCCACCTGGG	177
2909	Qy	CCATCAACTGTGAATTCCTCAGCACCACTGCCCTTTTAGGAACGCTAAAGTCCTTTAAAGCAC	2968
178	Db	CCATCAACTGTGAATTCCTCAGCACCACTGCCCTTTTAGGAACGCTAAAGTCCTTTAAAGCAC	237
2969	Qy	TCAGAGCCACATCACTCTCTGCGTGAATCTGGGGGTTGTTTCTGTGGGTGAGAGATG	3028
238	Db	TCAGAGCCACATCACTCTCTGCGTGAATCTGGGGGTTGTTTCTGTGGGTGAGAGATG	287
3029	Qy	TGTTGCTGTGCCACACCCAGTACAGTCTCTCTGACCCCTTTGGGCTCTCTCTCCCTTGT	3088
298	Db	TGTTGCTGTGCCACACCCAGTACAGTCTCTCTCTGACCCCTTTGGGCTCTCTCTCCCTTGT	357
3089	Qy	ACTCTTCAGCTGGCACCTGTCTCCATCTGCCCTACATGATGGGTAACCTGTATCTTCTT	3148
358	Db	ACTCTTCAGCTGGCACCTGTCTCCATCTGCCCTACATGATGGGTAACCTGTATCTTCTT	417
3149	Qy	CCCTGTTTAGATTGTAAGCCTCCNTCTTGTATCCAGCCCTAGCCAGTGCCTGCACACA	3208
418	Db	CCCTGTTTAGATTGTAAGCCTCCGCTTTTGTATCCAGCCCTAGCCAGTGCCTGCACACA	477
3209	Qy	GGAACTGTGCAATAAAGGTTTATGGAACAGAAAAA	3255
478	Db	GGAACTGTGCAATAAAGGTTTATGGAACAGAAAAA	524

RESULT 5	562 bp	linear	EST 21-APR-2001
LOCUS	BG220572		
DEFINITION	RS740358 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.		
ACCESSION	BG220572		
VERSION	BG220572.1		
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		

FEATURES	source
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/db_xref="taxon:9606"
/cell_line="HT1080"

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Db 84 GCCTCCGCTTTGTATCCAGCCCTAGCCAGTCGCTGACACAGGAACCTGTGCACATA 25

QY 3225 AAGGTTTATGGAACAGAAAAA 3248

Db 24 AAGGTTTATGGAACAGAAAAA 1

RESULT 8

AI131339/c

LOCUS

DEFINITION

qcl8c08.x1 Soares fetal heart NBHH19W Homo sapiens cDNA clone

IMAGE:1709966 3', mRNA sequence.

AI131339

AI131339.1 GI:3601355

EST.

SOURCE

ORGANISM

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 421)

NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapsb@mail.nih.gov

This clone is available royalty-free through LLM; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

Insert Length: 364 Std Error: 0.00

Seq primer: -40m3 fwd. ET from Amersham.

FEATURES

Location/Qualifiers

1..421

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:1709966"

/sex="unknown"

/dev_stage="19 weeks"

/lab_host="DH10B (ampicillin resistant)"

/clone_lib="Soares fetal heart NBHH19W"

/note="Organ: heart; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', TGCTACCATCTGAAGTGGAGCGCGCATCTTTTCTTTTCTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by M.Fatima Bonaldo. This library was constructed from the same fetus as the fetal lung library, Soares fetal lung NBHH19W."

ORIGIN

Query Match 12.8%; Score 418.4; DB 9; Length 421;

Best Local Similarity 99.5%; Pred. No. 2.5e-66;

Matches 419; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2824 AACGGCAGTTGAGGGCAATGACCCCTTGAGGACACTGTGAGGGCTGACGGGAGATGC 2883

Db 421 AACGGCAGTTGAGGGCAATGACCCCTTGAGGACACTGTGAGGGCTGACGGGAGATGC 362

QY 2884 CAGCCATCACTCACTGCCACCTGGGCCATCACTGGAATCTCAGCACCATGTCCTTT 2943

Db 361 CAGCCATCACTCACTGCCACCTGGGCCATCACTGGAATCTCAGCACCATGTCCTTT 302

QY 2944 TAGGAACGTAAGTCTCTTTAAGCACCTCAGAAGCATACTCATCTCTCGCTGATCTGG 3003

Db 301 TAGGAACGTAAGTCTCTTTAAGCACCTCAGAGCCATACCTCATCTCTCGCTGATCTGG 242

QY 3004 GGGTTGTTCTGTGGGTGAGAGATGTTGCTGTGCCACCCAGTACAGTTCCTCTCT 3063

Db 241 GGGTTGTTCTGTGGGTGAGAGATGTTGCTGTGCCACCCAGTACAGTTCCTCTCT 182

QY 3064 GACCCCTTGGCTCTCTCTTCTTCTTGTACTCTTCAGCTGCACCTGCTCAATCTTGCCTAC 3123

Db 181 GACCCCTTGGCTCTCTCTTCTTCTTGTACTCTTCAGCTGCACCTGCTCAATCTTGCCTAC 122

QY 3124 ATGATGGGTAACCTGTGATCTTCTTCCCTGTGTAGATTGTAAGCCTCCNTCTTTGTATCCC 3183

Db 121 ATGATGGGTAACCTGTGATCTTCTTCCCTGTGTAGATTGTAAGCCTCCGCTTTGTATCCC 62

QY 3184 AGCCCTAGCCAGTGCCTGACACAGGAACCTGTGCACATAAAGTTTATGGAACAGAA 3243

Db 61 AGCCCTAGCCAGTGCCTGACACAGGAACCTGTGCCAATAAAGTTTATGGAACAGAA 2

QY 3244 A 3244

Db 1 A 1

RESULT 9

BB626584

LOCUS

DEFINITION

BB626584 RIKEN full-length enriched, adult male diencephalon Mus musculus cDNA clone 9330210123 5', mRNA sequence.

ACCESSION

VERSION

BB626584

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 664)

Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y.

RIKEN Mouse ESTs (Arakawa, T., et al. 2001)

Unpublished (2001)

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Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

wagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and Hayashizaki, Y.

Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)

Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

GAATTGGCAGAG 3', adaptor sequence: 5'
CTCGAGTTTTTTTTTTTTTTTTTTT 3', Average insert size: 1.0 kb."

ORIGIN

Query Match 12.3%; Score 401.4; DB 9; Length 422;
Best Local Similarity 98.6%; Pred. No. 3.3e-63;
Matches 416; Conservative 0; Mismatches 2; Indels 4; Gaps 1;

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2903 CCTGGG-CCATCAACTGTGAATTCACAGA-CCAGTGGCTTTTAGGAACGTAAAGTCTCT 2960
Db ||||| 284
343 CCCGGGCCCATCAACTGTGAATTCACAGACCAGTGGCTTTTAGGAACGTAAAGTCTCT 284
2961 TTAAGCACTCAGAAGCCATACCTCATCTCTCTGGCTGATCTGGGGGTTGTTTCTGGGT 3020
Db ||||| 224
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Db ||||| 164
223 GAGAGATGTTGCTGGCCACCCAGTACAGTCTCTCTCTGACCCCTTTGGCTCTTCT 164
3081 TCCTTTGTACTCTCAGCTGGCAGCTGCTCCATCTGCGCTACATGATGGGTAACGTGA 3140
Db ||||| 104
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3141 TCCTTTCTCCCTGTAGATGTAAGCTCCNTCTTTGATCCAGCCCTAGCCAGTGC 3200
Db ||||| 44
103 TCCTTTCTCCCTGTAGATGTAAGCTCCNTCTTTGATCCAGCCCTAGCCAGTGC 44
3201 CTGACACAGGAAGTGTGCAATTAAGGTTTATGGAACAGA 3241
Db ||||| 3
43 CTGACACNGGAAGTGTGCAATTAAGGTTTATGGAACAGA 3

RESULT 11
AA968560/c
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DEFINITION
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mRNA sequence.
ACCESSION
AA968560.1 GI:3143740
VERSION
AA968560
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 422)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov
Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: Stratagene, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert length: 1745 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 396.
Location/Qualifiers
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/clone="IMAGE:1592181"
/sex="mixed"
/tissue type="kidney tumor"
/lab_host="SOLR (kanamycin resistant)"
/clone_lib="NCI CGAP_Kid6"
/notes="Organ: kidney; Vector: Bluescript SK-; Site 1:
EcORI; Site 2: XhoI; Cloned unidirectionally. Primer:
Oligo dt. Pooled kidney tumors. 5' adaptor sequence: 5'

FEATURES
source

AA9176 448 bp mRNA linear EST 22-JAN-1999
YQ18q02.r1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone
IMAGE:274346 5', mRNA sequence.
H49176
H49176.1 GI:989017
EST.
ACCESSION
H49176
VERSION
H49176
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 448)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Maizra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, P.,
Trevisan, E., Waterston, R., Williamson, A., Wohlmann, P. and
Wilson, R.
The WashU-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 585
High quality sequence stops: 362
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 585 Std Error: 0.00

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 21, 2004, 10:14:56 ; Search time 1177 Seconds
(without alignments)
11766.462 Million cell updates/sec

Title: US-10-028-248A-210
Perfect score: 3260
Sequence: 1 99cagcagcagagcttcccc.....aaaaaaaaaaaaaaaaaaaaa 3260

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124039041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N Geneseq 29Jan04:*

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- 2: geneseqn1990s:*
- 3: geneseqn2000s:*
- 4: geneseqn2001as:*
- 5: geneseqn2001bs:*
- 6: geneseqn2002s:*
- 7: geneseqn2003as:*
- 8: geneseqn2003bs:*
- 9: geneseqn2003cs:*
- 10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	3259	100.0	3260	6	ABT08489 Human nov
2	3232.6	99.2	4576	6	ABA04662 Human Hya
3	3232.6	99.2	4642	7	ABX13822 cDNA enco
4	2999.8	92.0	8444	6	ABT08487 Human nov
5	2995.6	91.9	8495	6	ABT08488 Human nov
6	2853.2	87.5	4962	7	ABX13823 cDNA enco
7	2828.8	86.8	3625	7	Aaf87120 NOV9 codi
8	1936.8	59.4	4706	6	ABA04648 Rat Hyalu
9	1936.8	59.4	4706	7	ABX13821 cDNA enco
10	1778.6	54.6	2483	4	Aaf87119 NOV8 codi
11	1777	54.5	2512	4	Aaf87117 NOV6 codi
12	1721.2	52.8	2011	4	Aaf87113 NOV2 codi
13	1429.6	43.9	1804	4	Aaf87114 NOV3 codi
14	1347.4	41.3	1377	3	AAC76373 Human ORF
15	1227.4	37.7	1259	3	AAS7365 DNA enco
16	990.2	30.4	1624	4	Aaf87118 NOV7 codi
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19	537	16.5	722	6	AAS62772 cDNA sequ
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27	248	7.6	1522	3	AAAS7363	DNA enco
28	247.4	7.6	395	8	ACH29524	Human adu
29	187.4	5.7	1482	7	ACA55632	Human sig
30	143	4.4	473	8	ACH15198	Human adu
31	135	4.1	420	8	ACH21247	Human adu
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35	81.4	2.5	1144	9	ADE25720	Human cDN
36	81.4	2.5	1414	2	AAQ27190	Tumour ne
37	81.4	2.5	1414	2	AAV71778	Tumour ne
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41	81.4	2.5	1422	7	ABX76382	Lung canc
42	81.4	2.5	1728	7	ABX63445	Human cDN
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44	78.2	2.4	1414	6	ABL68341	Kidney ca
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ALIGNMENTS

RESULT 1

ABT08489

ID ABT08489 standard; cDNA; 3260 BP.

XX

AC ABT08489;

DT 28-NOV-2002 (first entry)

DE Human novel protein NOV1c coding sequence SEQ ID NO: 210.

KW Human; NOVX; single nucleotide polymorphism; SNP; anti-HIV; cytostatic;
 KW antiarteriosclerotic; antidiabetic; antiasthmatic; antiinflammatory;
 KW haemostatic; hypotensive; neuroprotective; anorectic; nootropic;
 KW antidepressant; immunosuppressive; antibacterial; antiparasitic;
 KW viricide; tranquilizer; anticonvulsant; osteopathic; analgesic;
 KW antiparkinsonian; dermatological; antiinfertility; cerebroprotective;
 KW antiaddictive; gene; ss.
 XX Homo sapiens.

EH Key Location/Qualifiers
 FT variation replace(887,C)

FT variation /*tag= a

FT variation replace(1034,T)

FT variation /*tag= b

XX variation replace(1223,T)

XX /*tag= c

PN WO200259315-A2.

XX 01-AUG-2002.

PD 19-DEC-2001; 2001WO-US050076.

PF 19-DEC-2000; 2000US-0256619P.

PR 19-JAN-2001; 2001US-0262959P.

PR 28-FEB-2001; 2001US-0272408P.

PR 20-APR-2001; 2001US-0285189P.

PR 26-JUL-2001; 2001US-0308039P.

PR 09-AUG-2001; 2001US-0311266P.

XX (CURA-) CURAGEN CORP.

PA Shimkets RA, Patturajan M, Vernet CAM, Casman SJ, Malyankar U;

XX Shenoy S, Spytek RA, Gargolli E, Miller C, Boldog F, Li L;

PI Taupier Ru, Kekuda R, Smithson G, Zerhusen BD, Liu X, Colman SD;

PI	Tchernev V, Si J, Edinger S, Stone D, Sciore P, Millet I; Rothenberg M;	QY	601	TGTTCAACACAGACAAACAGCTGAAGGAGTATTGAAGTTTCATGTATACGAG
PI		Db	601	
DR	WPI; 2002-666903/71.	QY	661	ATGCCAAGGTTTACCTGTGGATCTCCACATCCATCCCTGCGAAGACCTTCGAAGGTT
DR	P-PSDB; ABJ10588.	Db	661	
XX	New isolated NOVX polypeptides and polynucleotides, useful for preventing, diagnosing or treating NOVX-associated disorders e.g. diabetes, Crohn's disease, atherosclerosis, cancer, Huntington's disease or Alzheimer's disease.	QY	721	CAGACTGAGTGTGAAATGTGGAGCTGGCAGGAGCATCGGTGACCTCTTTCTGAATGGCC
PT		Db	721	
PT		QY	781	AAACCTGCAGAAATCTGCAGCGGAGCTCTTTTGACCTGGGTGGCTACGGCAATG
PT		Db	781	
PS	Claim 42; Page 24-25; 363pp; English.	QY	841	ACTGTCGTGATTTGATCCACCTGGGGGGCGCTGTGACACCTTTACTTCTTCGATG
XX	The present invention provides the protein and coding sequences of several novel human proteins, designated NOVX. These can be used in the treatment of diseases such as cancers, Hodgkin's disease, von Hippel-Lindau syndrome, Alzheimer's disease, stroke, tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, cerebral palsy, epilepsy, Lesch-Nyhan syndrome, multiple sclerosis, ataxia, telangiectasia, leukodystrophies, addiction, anxiety, depression, pain, obesity, Crohn's disease, osteoporosis, inflammatory bowel disease, infertility, atherosclerosis, hypertension, scleroderma, haemophilia, diabetes, pancreatitis, autoimmune disease, asthma, arthritis, immunodeficiencies, HIV, viral, bacterial or parasitic infections, or graft-versus-host disease. The present sequence is a coding sequence of the invention	QY	901	CCTCGGGGAGTGTGGAGCTGTGCAATCTCCAGCTGCCAAGTGGAGTAAACCAA
XX		Db	901	
XX		QY	961	AGGGTGTGAAGCAGAAAGTGTCTTCTACACCTGCCCTTCAAGAGGAACTTGGAGGCTGCC
XX		Db	961	
SQ	Sequence 3260 BP; 774 A; 886 C; 850 G; 749 T; 0 U; 1 Other;	QY	1021	GGGAGCGTGCAGCTGTGATACAGATCCCGAGTGTGCAAGGCTACTTCCGGCGAG
	Query Match 100.0%; Score 3259; DB 6; Length 3260;	Db	1021	
	Best Local Similarity 100.0%; Pred. No. 0;	QY	1081	ACTGTCAGGCTTCCCTGGAGGACCAAGATGCCCGGTGTAATTAACGGGGTGTCTGCTTG
	Matches 3260; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Db	1081	
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Db	1 GGACAGCAGCAGGAGCTTCCAGAAACCCGAAACCTTCCAGTATTCTTCCAGTTCCAGG 60	Db	1141	
QY	61 AGCATTTCTGAAAGATCTGGTGGCCAGGCCCTTCACTGTTTTTGACCTTTATCTG 120	QY	1201	AGATGTCGTGGCCGGGAGATTTCGGGCTGATTTGCTGCTGCTGCTGCTGCTGCTGCTG
Db	61 AGCATTTCTGAAAGATCTGGTGGCCAGGCCCTTCACTGTTTTTGACCTTTATCTG 120	Db	1201	
QY	121 CAGCCTTTGATGAGGAAGCTCGGGTTAAAGACTGGGACAAATACGGTTTAAATGCCCCAGG 180	QY	1261	GACAGTGCATGATGTCATCAGGGCTCCGGGCTGAGTCCCTCTGTGAAAACGGGCTGGACAG
Db	121 CAGCCTTTGATGAGGAAGCTCGGGTTAAAGACTGGGACAAATACGGTTTAAATGCCCCAGG 180	Db	1261	
QY	181 TTCTTCGGTACATGTTGGTGGCTGCCACAGCTGCTTCTGGAACCTTGAATTCATCT 240	QY	1321	GCCCTCTGTTGACACTCAGGCAAGTTTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTC
Db	181 TTCTTCGGTACATGTTGGTGGCTGCCACAGCTGCTTCTGGAACCTTGAATTCATCT 240	Db	1321	
QY	241 CAAATGCTACTTCCCTCCAGGAGAGCCAAATAGTCACTCCGCTCTCAGAGCAGCGTGT 300	QY	1381	ATGCCACCTGTAAGAGAAACACAGCTGTGAGTGTAACTGGATTATGAGGTGACGGA
Db	241 CAAATGCTACTTCCCTCCAGGAGAGCCAAATAGTCACTCCGCTCTCAGAGCAGCGTGT 300	Db	1381	
QY	301 ATATAAATAAAGGCTAAGATCATATCCAGTGATATCATAGTACTAATGGGATTTGTC 360	QY	1441	TCACATGACAGTGTGGGATTTCTGCAAAACAGGACAAACGGGGCTCTGCAAAAGGTGCCCA
Db	301 ATATAAATAAAGGCTAAGATCATATCCAGTGATATCATAGTACTAATGGGATTTGTC 360	Db	1441	
QY	361 ATATCATAGCAAAATTTGCTATCCCAAAATTTGCTATCATCTCCCAAGACAACTCTG 420	QY	1501	GATGCTCCAGAAAGGCGACGAAAGTCTCTGCAAGCTCCAGAGGAGGATACAAAGGGGACG
Db	361 ATATCATAGCAAAATTTGCTATCCCAAAATTTGCTATCATCTCCCAAGACAACTCTG 420	Db	1501	
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QY	481 ACTTAATACAGGACTCAGGTTTCTGAGTGTCTATCCCGATCCATCCACACCCCGATCA 540	QY	1621	ACGCCACCTGTAAAGTGCACAGGCCCCGGGCAAGCAAAAGTGTGAAGTGTAAAGTCACTATG
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Db 3241 AAAAAAAAAAAAAAAAAAAAAA 3260

RESULT 2
ID ABA04662 standard; cDNA; 4576 BP.
AC ABA04662;
XX
XX
XX 22-FEB-2002 (first entry)
XX
XX Human Hyaluronic Acid Receptor for Endocytosis, HARE, coding sequence.
XX
XX HARE; Hyaluronic Acid Receptor for Endocytosis; hyaluronan; chondroitin;
XX chondroitin sulphate; extracellular matrix; cartilage; skin;
XX vitreous humour; endocytic receptor; glycosaminoglycan; human; ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
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XX /product= "Human HARE"
XX /note= "No start codon given"
XX
XX WO200181544-A2.
XX
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XX 25-APR-2001; 2001WO-US013403.
XX
XX 25-APR-2000; 2000US-0199538P.
XX
XX 02-NOV-2000; 2000US-0245320P.
XX
XX (WEIG/) WEIGEL P A.
XX PA (ZHOU/) ZHOU B.
XX PA (WEIG/) WEIGEL J A.
XX
XX Weigel PA, Zhou B, Weigel JA;
XX
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DR WPI; 2002-049271/06.
DR P-PSDB; AAM47684.
XX
PT New mammalian hyaluronic acid receptor for endocytosis, useful e.g. for
PT identifying agents that inhibit binding to hyaluronic acid, and related
PT nucleic acid.
XX
PS Claim 49; Fig 33; 263pp; English.
XX
CC The present invention relates to sequences for rat and human HARE
CC (Hyaluronic Acid Receptor for Endocytosis, ABA04648, ABA04662, AAM47675
CC and AAM47684). HARE can bind specifically to at least one of hyaluronic
CC acid (HA, also known as hyaluronan), chondroitin (C) or chondroitin
CC sulphate (CS). HA is an extracellular matrix component of all tissues, in
CC particular cartilage, skin and vitreous humour. HARE is the endocytic
CC receptor responsible for removing HA and other glycosaminoglycans from
CC the circulation. The present sequence is the coding sequence for human
CC HARE
XX
SQ Sequence 4576 BP; 1127 A; 1193 C; 1203 G; 1053 T; 0 U; 0 Other;
Query Match 99.2%; Score 3232.6; DB 6; Length 4576;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 3238; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
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67 TCGTGAAGAGCTCGGTGCGGCCAGGCCCTTCACTGTTTTTGCACCTTTATCTGAGCCT 126
1388 TCGTGAAGAGCTCGGTGCGGCCAGGCCCTTCACTGTTTTTGCACCTTTATCTGAGCCT 1447
127 TTGATGAGAGCTCGGTGCGGCCAGGCCCTTCACTGTTTTTGCACCTTTATCTGAGCCT 186
1448 TTGATGAGAGCTCGGTGCGGCCAGGCCCTTCACTGTTTTTGCACCTTTATCTGAGCCT 1507
187 GGTACCATCTGTCGCTCCAGCAGCTGCTTCTGGAACCTTGAATTTGATCTCAAATG 246
1508 GGTACCATCTGTCGCTCCAGCAGCTGCTTCTGGAACCTTGAATTTGATCTCAAATG 1567
247 CTACTTCCCTCCAAAGGAGCCAAATAGTATCATCTCGTCTCTCAGAGCAGCGTGTATATA 306
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307 ATAAATAGGCTAAGATCATATCAGTGTATCATCAGTACTAATGGGATTTTCATATCA 366
1628 ACAATAAGGCTAAGATCATATCAGTGTATCATCAGTACTAATGGGATTTTCATATCA 1687
367 TAGACAAATTTGCTATCTCCAAATTTTCTTATCATCTCCAAAGCAACTCTGGAAGAA 426
1688 TAGACAAATTTGCTATCTCCAAATTTTCTTATCATCTCCAAAGCAACTCTGGAAGAA 1747
427 TTCTGCAAAATCTTACGACTTTGGCAACAAATGGCTPACATCAAAATTTAGCAACTTAA 486
1748 TTCTGCAAAATCTTACGACTTTGGCAACAAATGGCTPACATCAAAATTTAGCAACTTAA 1807
487 TACAGACTCAGTTTGTGCTGAGTGTATCATCCGATCCCATCCACCCAGTCACTCTCT 546
1808 TACAGACTCAGTTTGTGCTGAGTGTATCATCCGATCCCATCCACCCAGTCACTCTCT 1867
547 TCTGGCCCAACGACCAAGCCCTCCATGCTTACCTGCTGAAACAAAGGACTTCTCTTTCA 606
1868 TCTGGCCCAACGACCAAGCCCTCCATGCTTACCTGCTGAAACAAAGGACTTCTCTTTCA 1927
607 ACCAAGACAAAGGACAGCTGAAGAGTATTTGAAGTTTCATGTGATACAGATGCCA 666
1928 ACCAAGACAAAGGACAGCTGAAGAGTATTTGAAGTTTCATGTGATACAGATGCCA 1987
667 AGGTTTTAGCTGTGATCTTCCACATCCAGTCCCTGGAAGCCCTGCAAGGTTTCAGAGC 726
1988 AGGTTTTAGCTGTGATCTTCCACATCCAGTCCCTGGAAGCCCTGCAAGGTTTCAGAGC 2047

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Db 3188 GTGCCAACAGCTGCGAACATGGCAACCTACAAACAGCTCTCTCTATGCCCCAGAGGCCCA 3247
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Db 4448 ATGGGTAACTGTGATCTTTCTTCCCTGTGTAGATTGTGAAGCTCTCTTTGTATCCAGC 4507
QY 3187 CCTAGCCAGTGCCTGACACAGGAACCTGTGCACAATAAAGCTTTATGGAACAGAAAAA 3246
Db 4508 CCTAGCCAGTGCCTGACACAGGAACCTGTGCACAATAAAGCTTTATGGAACAGAAAAA 4567
QY 3247 AAAAAAAA 3254
Db 4568 AGTCAACA 4575
RESULT 3
ABX13822
ID ABX13822 standard; cDNA; 4642 BP.
XX
AC ABX13822;
XX
DT 19-FEB-2003 (first entry)
XX
DE cDNA encoding human 190kDa Hyaluronan receptor for endocytosis #1.
XX
KW Hyaluronan receptor for endocytosis; HARE; hyaluronan; HA; CD;
KW chondroitin molecule; chondroitin sulphate; CDS; targeting; metastasis;
XX tumour; gene therapy; human; gene; ss.
OS Homo sapiens.
Key Location/Qualifiers
CDS 1..4251
/tag= a
/product= "HARE"
/note= "Hyaluronan receptor for endocytosis"
/partial
/note= "No start codon given"
XX WO2002B6093-A2.
XX
XX 31-OCT-2002.
XX 25-APR-2002; 2002WO-US013209.
XX 25-APR-2001; 2001US-00842930.
XX 25-APR-2001; 2001US-0286468P.
XX (WEIG/) WEIGEL P H.
XX (WEIG/) WEIGEL J A.
XX Weigel PH, Weigel JA;
XX
XX WPI; 2003-093126/08.
XX P-PSDB; ABG72499.
XX
XX Targeting compounds e.g. chemotherapeutic agent to cell of subject
XX expressing functional active hyaluronan receptor for endocytosis of HARE,
XX by using hyaluronan, HARE, and/or monoclonal antibody that binds to HARE
XX epitope.
XX

PS Example; Fig 9A; 167pp; English.

XX The invention describes a method of targeting a compound to a cell or
CC tissue of an individual expressing a functionally active hyaluronan (HA)
CC receptor for endocytosis (HARE) or a cell that does not express
CC functionally active HARE. The method involves using HA molecule, a
CC chondroitin molecule (CD), a chondroitin sulphate (CDS) molecule, and/or
CC a monoclonal antibody raised against a HA-binding domain of HARE. The
CC method is useful for targeting a compound, preferably a chemotherapeutic
CC agent or a radioisotope to cell of an individual, especially a human,
CC expressing HARE on its surface (e.g. gene therapy). Also described is a
CC method useful for preventing interaction between a cell having at least
CC one of a HA coat, a CD coat and CDS coat and a cell expressing HARE on
CC its surface. This second method is useful for preventing metastasis by
CC preventing interaction between tumour cells having HA, CD or CDS coat and
CC non-tumour cells expressing HARE on its surface. The invention also
CC describes a method useful for detecting the presence of HA, CD and CDS in
CC a biological fluid. This sequence encodes the human 190kDa Hyaluronan
CC receptor for endocytosis (HARE)

XX Sequence 4642 BP; 1141 A; 1215 C; 1216 G; 1070 T; 0 U; 0 Other;

Query Match 99.2%; Score 3232.6; DB 7; Length 4642;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 3238; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY	7	AGCAGAGCTTCCCAAGAACCCGAAACCTCCAGTATTTCTTCCAGTTGCAGGACATT	56
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QY	67	TGCTGAAGAGATCTGGTCGCCGCCAGGCCCTTCACTGTTTTTGACCTTTATCTGCAGCCT	126
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QY	127	TTGATCAGGAGCTCGGGTTAAAGACTGGGACAAATACGGTTTAAATGCCCCAGGTTCTTC	186
DB	1514	TTGATCAGGAGCTCGGGTTAAAGACTGGGACAAATACGGTTTAAATGCCCCAGGTTCTTC	1573
QY	187	GGTACCATGTGTCGCTGCCACCACTGCTTCTGGAACCTGAAATGATCTCAATG	246
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QY	247	CTACTTCCCTCAAGGAGACCAATAGTATCATCTCCGTCTCTCAGAGCAGGGTATATAA	306
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QY	487	TACAGACTCAGGTTTGTGAGTGTATCATCCGATCCATCCACACCCAGTCACTCTCT	546
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QY	547	TCCTGCCCAACGACCAAGCCCTCATGCCCCTACTCTGCTGAACCAACAGGACTTCCCTGTCA	606
DB	1934	TCCTGCCCAACGACCAAGCCCTCATGCCCCTACTCTGCTGAACCAACAGGACTTCCCTGTCA	1993
QY	607	ACCAAGACAAACAGGACCAAGCTGAAGGAGTATTTGAAGTTTCATGTGATACGAGATGCCA	666
DB	1994	ACCAAGACAAACAGGACCAAGCTGAAGGAGTATTTGAAGTTTCATGTGATACGAGATGCCA	2053
QY	667	AGGTTTGTGAGTCTTCCCATCATCTGCTGGAAGACCCCTGCAAGGTTTCAGAGC	726
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QY	847	TGCTGATTTGATCCCACTTGGGGGGCGCTGTGACACCTTTTACTACTTTTCGATGCTCGG	906
DB	2234	TGCTGATTTGATCCCACTTGGGGGGCGCTGTGACACCTTTTACTACTTTTCGATGCTCGG	2293
QY	907	GGGAGTGTGGGAGCTGTCTCAATATCTCCAGCTGCCCAAGGTGGAGTAAACCAAGGGTGG	966
DB	2294	GGGAGTGTGGGAGCTGTCTCAATATCTCCAGCTGCCCAAGGTGGAGTAAACCAAGGGTGG	2353
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DB	2354	TGAAGCAGAAAGTGTCTCTCAACCTGCCCTTCAAGAGGAACCTGGAAGGCTGCCGGGAGC	2413
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QY	1147	ACTCGGCCACCCGAGAGTGAATGCAACACCGGCTTCAATGGGACGGCGTGTGATGTT	1206
DB	2534	ACTCGGCCACCCGAGAGTGAATGCAACACCGGCTTCAATGGGACGGCGTGTGATGTT	2593
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DB	2654	GCGATGATGGCATCACGGGCTCCGGGACGTGCTCTGTGAAACGGGGTGGACAGGCCCT	2713
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DB	2774	CTGTGAAGAGAACACAGTGTGAGTGTAACTGATTAATGAAGTGAACGGAATCACAT	2833
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DB	3074	ATGGGCTGAATCTGTGAGCGGAGCAGCTGCCCATTCACCGCTGCTTACAGAGCAATGGGC	3133
QY	1747	AGTGCCATGACAGACGCAAAATGTGTCGACCTCCACTTCCAGGATACCACTGTGGGGTGT	1806
DB	3134	AGTGCCATGACAGACGCAAAATGTGTCGACCTCCACTTCCAGGATACCACTGTGGGGTGT	3193

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Db |||||||
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QY 4034 ACTCCTACTTTCGATAAACCGGAGAACATCGGCTTCCAGATTTTGAATCGGAAGG 4093
Db |||||||
QY 2707 ACATTAAATGTTGAGCTCTTGGCAGCAGCAGCTGAGAAATCTCGAACCCCTTGTATG 2766
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QY 4214 GGCAGCTTGGGCAATGAGACCCCTTGGAGCACTGTGAGGGGCTGGAGCGGAGATGCCAG 4273
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QY 2887 CCATCACTCACTGCCACCTGGGCCATCAACTGTGAAATTTCTCAGCACCACTTGGCTTTAG 2946
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Db 4274 CCATCACTCACTGCCACCTGGGCCATCAACTGTGAATTTCTCAGCACCACTTGCCTTTTAG 4333
QY 2947 GAACGTAAAGTCTCTTTAAGCACTCAGAAGCCATACCTCATCTCTGCGCTGATCTGGGG 3006
Db 4334 GAACGTAAAGTCTCTTTAAGCACTCAGAAGCCATACCTCATCTCTCTGCGCTGATCTGGGG 4393
QY 3007 TTGTTTCTGTGGGTGAGAGATGTGTGTGTGTCGCCACCCAGTACAGCTTCTCTCTCTGAC 3066
Db 4394 TTGTTTCTGTGGGTGAGAGATGTGTGTGTGTCGCCACCCAGTACAGCTTCTCTCTCTGAC 4453
QY 3067 CCTTTGGCTCTTCTCTTTTACTTCTTCTCAGCTGGGACCTGCTCAATCTTGCCTTACATG 3126
Db 4454 CCTTTGGCTCTTCTCTTTTACTTCTTCTCAGCTGGGACCTGCTCAATCTTGCCTTACATG 4513
QY 3127 ATGGGTAACTGTGATCTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 3186
Db 4514 ATGGGTAACTGTGATCTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 4573
QY 3187 CCTTAGCCAGTCCCTGACACAGGAACTGTGCAATAAAGGTTTATGGAACAGAAAAA 3246
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QY 3247 AAAAAAAA 3254
Db 4634 AGTCAACA 4641

RESULT 4
ABT08487
ID ABT08487 standard; cDNA; 8444 BP.
XX
AC ABT08487;
XX
DT 28-NOV-2002 (first entry)
XX
DE Human novel protein NOV1a coding sequence SEQ ID NO: 1.
XX
KW Human; NOVX; single nucleotide polymorphism; SNP; anti-HIV; cytostatic;
KW antiarteriosclerotic; antidiabetic; antiasthmatic; antiinflammatory;
KW haemostatic; hypotensive; neuroprotective; anorectic; nootropic;
KW antidepressant; immunosuppressive; antibacterial; antiparasitic;
KW virucide; tranquilizer; anticonvulsant; osteopathic; analgesic;
KW antiparkinsonian; dermatological; antifertility; cerebroprotective;
KW antiaddictive; gene; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT variation replace(4185,C)
FT FT /*tag= a
FT variation replace(4524,C)
FT FT /*tag= b
FT variation replace(4654,A)
FT FT /*tag= c
FT variation replace(4671,G)
FT FT /*tag= d
FT variation replace(4820,C)
FT FT /*tag= e
XX
XX WO200259315-A2.
XX
XX PD 01-AUG-2002.
XX
XX PD 19-DEC-2001; 2001WO-US050076.
XX
XX PD 19-DEC-2000; 2000US-0256619P.
XX
XX PD 19-JAN-2001; 2001US-0262959P.
XX
XX PD 28-FEB-2001; 2001US-0272408P.
XX
XX PD 20-APR-2001; 2001US-0285189P.
XX
XX PD 26-JUL-2001; 2001US-0308039P.
XX
XX PD 09-AUG-2001; 2001US-0311266P.
XX

(CURA-) CURAGEN CORP.

PA Shinkets RA, Patturajan M, Vernet CAM, Casman SJ, Malyankar U;
PI Shenoy S, Spytek KA, Gangolli E, Miller C, Boldog F, Li L;
PI Taupier RJ, Kekuda R, Smithson G, Zerhusen BD, Liu X, Colman SD;
PI Tchernev V, Si J, Edinger S, Stone D, Sciore P, Millet I;
PI Rothenberg M;
XX WPI; 2002-666903/71.
DR P-PSDB; ABU10586.
XX New isolated NOVX polypeptides and polynucleotides, useful for
PT preventing, diagnosing or treating NOVX-associated disorders e.g.
PT diabetes, Crohn's disease, atherosclerosis, cancer, Huntington's disease
PT or Alzheimer's disease.

Claim 8; Page 17-19; 363pp; English.

XX The present invention provides the protein and coding sequences of
CC several novel human proteins, designated NOVX. These can be used in the
CC treatment of diseases such as cancers, Hodgkin's disease, Von Hippel-
CC Lindau syndrome, Alzheimer's disease, stroke, tuberous sclerosis,
CC hypercalcaemia, Parkinson's disease, Huntington's disease, cerebral
CC palsy, epilepsy, Lesh-Nyhan syndrome, multiple sclerosis, ataxia
CC telangiectasia, leukodystrophies, addiction, anxiety, depression, pain,
CC obesity, Crohn's disease, osteoporosis, inflammatory bowel disease,
CC infertility, atherosclerosis, hypertension, scleroderma, haemophilia,
CC diabetes, pancreatitis, autoimmune disease, asthma, arthritis,
CC immunodeficiencies, HIV, viral, bacterial or parasitic infections, or
CC graft-versus-host disease. The present sequence is a coding sequence of
CC the invention

XX Sequence 8444 BP; 2251 A; 2105 C; 2147 G; 1929 T; 0 U; 12 Other;

Query Match 92.0%; Score 2999.8; DB 6; Length 8444;
Best Local Similarity 96.1%; Pred. No. 0;
Matches 3128; Conservative 0; Mismatches 18; Indels 108; Gaps 1;

QY 7 AGCAGAGCTTCCCAAGAACCGAAACCTCCAGTATTCTTCCAGTTGCCAGGACATT 66
DB 5279 ATCAGAGCTTCCCAAGAACCGAAACCTCCAGTATTCTTCCAGTTGCCAGGACATT 5338
QY 67 TCGTGAAGATCTGGTCGGCCAGGCCCTTCACTCTTTTGGACCTTTATCTGCAGCCT 126
DB 5339 TCGTGAAGATCTGGTCGGCCAGGCCCTTCACTCTTTTGGACCTTTATCTGCAGCCT 5398
QY 127 TTGATCAGGAAGCTCGGGTTAAAGACTGGGACAAATACGGTTTAAATGCCAGGTTCTTC 186
DB 5399 TTGATCAGGAAGCTCGGGTTAAAGACTGGGACAAATACGGTTTAAATGCCAGGTTCTTC 5458
QY 187 GGTACCATGTGGTCGGCTGCCACGAGCTGTTCTGGAACCTGAAATTGATCTCAATG 246
DB 5459 GGTACCATGTGGTCGGCTGCCACGAGCTGTTCTGGAACCTGAAATTGATCTCAATG 5518
QY 247 CTACTTCCCTCCCAAGAGAGCCAAATGATCATCTCCGCTCTCTCAGAGCAGGTTATATA 306
DB 5519 CTACTTCCCTCCCAAGAGAGCCAAATGATCATCTCCGCTCTCTCAGAGCAGGTTATATA 5578
QY 307 ATAATAGGCTAAGATCATATCAGTGATATCATCTAGTACTAATGGGATTTGTCATATCA 366
DB 5579 ATAATAGGCTAAGATCATATCAGTGATATCATCTAGTACTAATGGGATTTGTCATATCA 5638
QY 367 TAGACAAATTTGCTATCTCCCAAAATTTGCTTATCATCTCCAAAGACAACTCTGGAAGAA 426
DB 5639 TAGACAAATTTGCTATCTCCCAAAATTTGCTTATCATCTCCAAAGACAACTCTGGAAGAA 5698
QY 427 TTCTGCAAAATCTTACGACTTTTGGCAACAAATGCTATCATCAAAATTTAGCAACTTAA 486
DB 5699 TTCTGCAAAATCTTACGACTTTTGGCAACAAATGCTATCATCAAAATTTAGCAACTTAA 5758
QY 487 TACAGGACTCAGGTTTGTGAGTGATCATACCGATCCCATCCACCCAGTCACTCTCT 546
DB 5759 TACAGGACTCAGGTTTGTGAGTGATCATACCGATCCCATCCACCCAGTCACTCTCT 5818

Qy	1627	CCTGTAAGATGACAGGCCCGGGGCAAGCAAAAGTGTGAGTGTAAAGATCACTATGTGCGAG	1688
Db	6899	CCTGTAAGATGACAGGCCCGGGCAAGCAAAAGTGTGAGTGTAAAGATCACTATGTGCGAG	6958
Qy	1687	ATGGGCTGAACCTGTGAGCCGGAGCAGCTGCCCATTTGACCGCTGTACAGGACAAATGGC	1746
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Qy	1747	AGTGCCATGACAGCGCCAAATGTGTGCACCTTCCACTTCCAGGATACCACCTGTTGGGGTGT	1806
Db	7019	AGTGCCATGACAGCGCCAAATGTGTGCACCTTCCACTTCCAGGATACCACCTGTTGGGGTGT	7078
Qy	1807	TCCATCTACCGTCCCCACTGGCCCAAGCTAATAGCTGAACCTTTGACAAAGCCAGAGAGCCCT	1866
Db	7079	TCCATCTACCGTCCCCACTGGCCCAAGCTAATAGCTGAACCTTTGACAAAGCCAGAGAGCCCT	7138
Qy	1867	GTGCCAACGAAGCTGCCACCATGCAACCTACACACAGCTCTCCTATGCCAGAAAGGCCA	1926
Db	7139	GTGCCAACGAAGCTGCCACCATGCAACCTACACACAGCTCTCCTATGCCAGAAAGGCCA	7198
Qy	1927	AGTACCACCTGTGTCTACAGAGGCTGGCTGGAGACCGGGCGGGTTGCCCTACCCCAACAGCCCT	1986
Db	7199	AGTACCACCTGTGTCTACAGAGGCTGGCTGGAGACCGGGCGGGTTGCCCTACCCCAACAGCCCT	7258
Qy	1987	TCGGCTCCAGAACTGTGGCTCTGGTGTGGTATGAGCTATGGAATATGGAACCTTAGACCCA	2046
Db	7259	TCGGCTCCAGAACTGTGGCTCTGGTGTGGTATGAGCTATGGAATATGGAACCTTAGACCCA	7318
Qy	2047	ACAAGAGTGAATGTGGGATGTCTTCGCTATCGGATGAAGATGTGAACCTGCACCTGCA	2106
Db	7319	ACAAGAGTGAATGTGGGATGTCTTCGCTATCGGATGAAGATGTGAACCTGCACCTGCA	7358
Qy	2107	AGGTGGCTATGTGGGAGATGGCTTCTCATGCACTGGGAACCTGCTGCAGGTCCTGATGT	2166
Db	7359	-----	7358
Qy	2167	CTTCCCTCCACTCAACAACCTTCTGACGGAAGTGTGGCTATTTCCAACAGCTCAGCTC	2226
Db	7359	-----GGAAGTGTGGCTATTTCCAACAGCTCAGCTC	7390
Qy	2227	GAGGCCGTGCATTTCTAGAACACTGACTGACTGCTCCATCCCGGGCAGCCCTTTTGTGC	2286
Db	7391	GAGGCCGTGCATTTCTAGAACACTGACTGACTGCTCCATCCCGGGCAGCCCTTTTGTGC	7450
Qy	2287	CACAGAACAGTGGGCTGGGGAGAAATGAGACCTTGTCTGGGGGGGACATCGAGCACACC	2346
Db	7451	CACAGAACAGTGGGCTGGGGAGNAATGAGACCTTGTCTGGGGGGGACATCGAGCACACC	7510
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Qy	2407	GGGTGGGAAGCAAGCTGCTCATCACTGCCAGCAGGACCCACCTCCAAACCGAGGAGACCA	2466
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Qy	2467	GGTTTGTGATGGAAGACCAATCTGCAGTGGGACATCTTTGGCTCCAATGGGATCATTC	2526
Db	7631	GGTTTGTGATGGAAGACCAATCTGCAGTGGGACATCTTTGGCTCCAATGGGATCATTC	7690
Qy	2527	ATGTCATTTCCAGGCCCTTTAAAGACACCCCTGCCCGCCGTGACCTTTGACCCACATGGCT	2586
Db	7691	ATGTCATTTCCAGGCCCTTTAAAGACACCCCTGCCCGCCGTGACCTTTGACCCACATGGCT	7750
Qy	2587	TGGGAGCAGGGATCTTTTGCCATCATCTGTGTGACTGGGGCTGTGTGCTTGGCTGCTT	2646
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Qy	2647	ACTCCTACTTTTCGATAAACCAGGAGAACAAATCGGCTTTCAGACATTTTGTAGTCGGAGAGG	2706
Db	7811	ACTCCTACTTTTCGATAAACCAGGAGAACAAATCGGCTTTCAGACATTTTGTAGTCGGAGAGG	7870
Qy	2707	ACATTAAATGTTCAGCTCTTTGGCAAGCAGCAGCTCGAGAATATCTCGAAACCCCTTGATG	2766

Db	7871	ACATTAATGTTGCAGCTCTTGCGAAGCAGCAGCCTGAGAAATATCTCGAACCCCTTGTA	7930
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Db	7931	AGAGCACAACCTCAGCTCCCCAGAACCTTCTCAGACCCCTTCAACGGACTCTGAAGAAC	7990
QY	2827	GGCAGCTTGAGGCAATGACCCCTTGAGGACACTGTGAGGSCCTGGACGGAGATGCCAG	2886
Db	7991	GGCAGCTTGAGGCAATGACCCCTTGAGGACACTGTGAGGSCCTGGACGGAGATGCCAG	8050
QY	2887	CCATCACTCACTGCCACCTGGGCCATCAACTGTGAATCTCAGCACCAAGTTGCCCTTTAG	2946
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QY	3067	CCTTTGGCTCTCTCTCTTTGTA	3126
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QY	3127	ATGGGTAACTGTGATCTTCTTCCTGTTAGATGTAAGCTCCTGATCCAGC	3186
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QY	3187	CCCTAGCCCACTGCTGACACAGAACTGTGCACATAAAGGTTTATGGAAACAGAAAA	3246
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ID	ABT08488 standard; cDNA; 8495 BP.		
XX			
AC	ABT08488;		
XX			
DT	28-NOV-2002 (first entry)		
XX			
DE	Human novel protein NOV1b coding sequence SEQ ID NO: 3.		
XX			
KW	Human; NOVX; single nucleotide polymorphism; SNP; anti-HIV; cytostatic;		
KW	antiarteriosclerotic; antidiabetic; antischmatic; antiinflammatory;		
KW	haemostatic; hypotensive; neuroprotective; anorectic; nootropic;		
KW	antidepressant; immunosuppressive; antibacterial; antiparasitic;		
KW	virucide; tranquilizer; anticonvulsant; osteopathic; analgesic;		
KW	antiparkinsonian; dermatological; antiinfertility; cerebroprotective;		
KW	antiaddictive; gene; ss.		
OS	Homo sapiens.		
XX			
PN	W0200259315-A2.		
XX			
PD	01-AUG-2002.		
XX			
PF	19-DEC-2001; 2001WO-US050076.		
XX			
PR	19-DEC-2000; 2000US-0256619P.		
PR	19-JAN-2001; 2001US-0262959P.		
PR	28-FEB-2001; 2001US-0272408P.		
PR	20-APR-2001; 2001US-0285189P.		
PR	26-JUL-2001; 2001US-0308039P.		
PR	09-AUG-2001; 2001US-0311266P.		
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QY 1738 ACAATGGGAGTGCCCATGAGACGCAAAATGTCGACTTCACATTCACAGGATACCACTG 1797
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QY 7051 ACAATGGGAGTGCCCATGAGACGCAAAATGTCGACTTCACATTCACAGGATACCACTG 7110
Db |||||
QY 1798 TTGGGGTGTTCATCTAGCTCCCACTGGGCAAGTATAGTGAAGTGAACCTTTGACAAAGCCA 1857
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Db |||||
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QY 2578 ACACCTGGCTTGGGAGCAGGATCTTTCTTTGGCATCATCTCTGCTGACTGGGCTGTGGCT 2637
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QY 7784 ACACCTGGCTTGGGAGCAGGATCTTTCTTTGCCATCATCTCTGCTGACTGGGCTGTGGCT 7843
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Db |||||
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Db 7904 CGGAAGGAGACATTAATGTTGCACTCTTGGCAAGCAGCAGCCTGAGAATATCTCGAACC 7963
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QY 8024 CTGAAGAACCGGAGCTTGAAGGCAATGACCCCTTGAGGACACTGTGAGGCGCTTGCACGGG 8083
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QY 2878 AGATGCCAGCATTCACTCAGTCCCACTGGGCACTAACTGTGAATTTCTCAGCACAGTT 2937
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QY 8084 AGATGCCAGCATTCACTCAGTCCCACTGGGCACTAACTGTGAATTTCTCAGCACAGTT 8143
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QY 8324 CCCTACATGATGGGTAACTGTGATCTTTCTTCCCTGTTAGATTGTAAGCCTCCCTCTTTG 8383
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QY 8384 TATCCAGCCCTAGCCAGTCCCTGACACAGGAATCTGTGCAACAATAAGGTTTATGGAA 8443
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Db |||||
RESULT 6
ABX13823
ID ABX13823 standard; cDNA; 4962 BP.
XX
AC ABX13823;
XX
DT 19-FEB-2003 (first entry)
XX
DE cDNA encoding human 190kDa Hyaluronan receptor for endocytosis #2.
XX
KW Hyaluronan receptor for endocytosis; HARE; hyaluronan; HA; CD;
KW chondroitin molecule; chondroitin sulphate; CDS; targeting; metastasis;
KW tumour; gene therapy; human; gene; ss.
XX
OS Homo sapiens.
XX
Key Location/Qualifiers
CDS 1..4962
FT /*tag= a
FT /product= "HARE"
FT /note= "Hyaluronan receptor for endocytosis"
FT /partial
FT /note= "No start codon given"
XX
XX MO200286093-A2.
XX
XX 31-OCT-2002.
XX
XX 25-APR-2002; 2002WO-US013209.
XX
XX 25-APR-2001; 2001US-00842930.
XX
XX 25-APR-2001; 2001US-0286468P.
XX
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PA (WEIG/) WEIGEL P H.
PA (WEIG/) WEIGEL J A.
XX Weigel PH, Weigel JA;
XX P-PSDB; ABG72514.
XX Targeting compounds e.g. chemotherapeutic agent to cell of subject
PT expressing functional active hyaluronan receptor for endocytosis of HARE,
PT by using hyaluronan, HARE, and/or monoclonal antibody that binds to HARE
PT epitope.
XX Example; Fig 9B; 167pp; English.
XX The invention describes a method of targeting a compound to a cell or
XX tissue of an individual expressing a functionally active hyaluronan (HA)
XX receptor for endocytosis (HARE) or a cell that does not express
XX functionally active HARE. The method involves using HA molecule, a
XX chondroitin molecule (CD), a chondroitin sulphate (CDS) molecule, and/or
XX a monoclonal antibody raised against a HA-binding domain of HARE. The
XX method is useful for targeting a compound, preferably a chemotherapeutic
XX agent or a radioisotope to cell of an individual, especially a human,
XX expressing HARE on its surface (e.g. gene therapy). Also described is a
XX method useful for preventing interaction between a cell having at least
XX one of a HA coat, a CD coat and CDS coat and a cell expressing HARE on
XX its surface. This second method is useful for preventing metastasis by
XX preventing interaction between tumour cells having HA, CD or CDS coat and
XX non-tumour cells expressing HARE on its surface. The invention also
XX describes a method useful for detecting the presence of HA, CD and CDS in
XX a biological fluid. This sequence encodes a longer version of the human
XX 190kDa Hyaluronan receptor for endocytosis (HARE) shown in ABG72499
XX (Encoded by AEX13822)
XX
SQ Sequence 4962 BP; 1249 A; 1277 C; 1311 G; 1125 T; 0 U; 0 Other;
Query Match 87.5%; Score 2853.2; DB 7; Length 4962;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2855; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 7 AGCAGAGCTTCCCAAGAACCCGAAACATTCACAGTATTTCTTCCAGTTTGCAGGACATT 66
Db 2105 ATCAGAGCTTCCCAAGAACCCGAAACATTCACAGTATTTCTTCCAGTTTGCAGGACATT 2164
QY 67 TCGTGAAGATCTGGTCCGCCAGCCCTTCACTGTTTTCACCTTTTTCACCTTTATCTGACGCT 126
Db 2165 TCGTGAAGATCTGGTCCGCCAGCCCTTCACTGTTTTCACCTTTTTCACCTTTATCTGACGCT 2224
QY 127 TTGATGAGGAAGCTCGGGTTAAAGACTGGGACAAATACGGTTTAAATGCCCCAGGTTCTTC 186
Db 2225 TTGATGAGGAAGCTCGGGTTAAAGACTGGGACAAATACGGTTTAAATGCCCCAGGTTCTTC 2284
QY 187 GGTACCATGTGTCGCTCCAGCAGCTGCTTCTGGAACCTGGAATTTGATCTCAATG 246
Db 2285 GGTACCATGTGTCGCTCCAGCAGCTGCTTCTGGAACCTGGAATTTGATCTCAATG 2344
QY 247 CTACTTCCCTCCAAAGAGACCAATAGTATCATCTCCGCTCTCAGACACGGTGTATATAA 306
Db 2345 CTACTTCCCTCCAAAGAGACCAATAGTATCATCTCCGCTCTCAGACACGGTGTATATAA 2404
QY 307 ATAATAAGGCTAAGATCATATCATATCATATCATATCATATCATATCATATCATATCA 366
Db 2405 ACATAAAGGCTAAGATCATATCATATCATATCATATCATATCATATCATATCATATCA 2464
QY 367 TAGACAAATGCTATCTCCGAAATTTGCTTATCATCTCCGAAAGACCACTCTGGAGAA 426
Db 2465 TAGACAAATGCTATCTCCGAAATTTGCTTATCATCTCCGAAAGACCACTCTGGAGAA 2524
QY 427 TTCTGCAAAATCTTAGACTTTTGGCAACAAACAAATGGCTACATCAAAATTTAGCACTTAA 486
Db 2525 TTCTGCAAAATCTTAGACTTTTGGCAACAAACAAATGGCTACATCAAAATTTAGCACTTAA 2584
QY 487 TACAGGACTCAGGTTTGTGAGTGTATCATCCGATCCCATCCACCCCGAGTCACTCTCT 546
Db 2585 TACAGGACTCAGGTTTGTGAGTGTATCATCCGATCCCATCCACCCCGAGTCACTCTCT 2644
QY 547 TCTGGCCCAACGACCAAGCCCTCCATGCGCTTACCTGCTGAACAAAGGACTTCTCTGTCA 606
Db 2645 TCTGGCCCAACGACCAAGCCCTCCATGCGCTTACCTGCTGAACAAAGGACTTCTCTGTCA 2704
QY 607 ACCAAGACCAACGACCAAGCTGAAGAGTATTTTGAAGTTTTCATGTGATACAGATGCCA 666
Db 2705 ACCAAGACCAACGACCAAGCTGAAGAGTATTTTGAAGTTTTCATGTGATACAGATGCCA 2764
QY 667 AGGTTTATAGCTGTGGATCTTCCACATCCACTGCTGGAAGACCCCTGCAAGGTTTCAGAGC 726
Db 2765 AGGTTTATAGCTGTGGATCTTCCACATCCACTGCTGGAAGACCCCTGCAAGGTTTCAGAGC 2824
QY 727 TGAGTGAATATGTGGAGCTGCGAGGACATCCGTCACCTCTTCTGAATGCCAAACCT 786
Db 2825 TGAGTGAATATGTGGAGCTGCGAGGACATCCGTCACCTCTTCTGAATGCCAAACCT 2884
QY 787 GCAGAAATGTGACGCGGAGCTTCTTGTGCTGCTGGCTTGGCTTACGCAATTTGACTGTC 846
Db 2895 GCAGAAATGTGACGCGGAGCTTCTTGTGCTGCTGGCTTGGCTTACGCAATTTGACTGTC 2944
QY 847 TGCTGATGATCCCAACCTTGGGGGCGCTGTGACACCTTTACTTACTTTCGATGCTCGG 906
Db 2945 TGCTGATGATCCCAACCTTGGGGGCGCTGTGACACCTTTACTTTCGATGCTCGG 3004
QY 907 GGGAGTGGGAGCTGTCAATATCCAGCTGCCAGGTCGCAAGGTGGAGTAAACCAAGGGTG 966
Db 3005 GGGAGTGGGAGCTGTCAATATCCAGCTGCCAGGTCGCAAGGTGGAGTAAACCAAGGGTG 3064
QY 967 TGAAGCAGAAGTGTCTTACAACTCTTCAAGAGGAACCTGGAAGGCTGCGGGAGC 1026
Db 3065 TGAAGCAGAAGTGTCTTACAACTCTTCAAGAGGAACCTGGAAGGCTGCGGGAGC 3124
QY 1027 GGTGACGCTGTGTATACAGATCCCAAGCTGCTGCAAGGGCTACTTTCGGGCGAGACTGTC 1086
Db 3125 GGTGACGCTGTGTATACAGATCCCAAGCTGCTGCAAGGGCTACTTTCGGGCGAGACTGTC 3184
QY 1087 AGGCTTCCCTCGAGGACCAAGTCCCGTGAATAACCCGGGTGCTCCCTTTGATCACT 1146
Db 3185 AGGCTTCCCTCGAGGACCAAGTCCCGTGAATAACCCGGGTGCTCCCTTTGATCACT 3244
QY 1147 ACTCGGCCACCCGAGAGTGAATGCAACACCGGCTTCAATGGGACGGCTGTGAGATGT 1206
Db 3245 ACTCGGCCACCCGAGAGTGAATGCAACACCGGCTTCAATGGGACGGCTGTGAGATGT 3304
QY 1207 GGTGCGGGGAGATTCGGGCTGATTTGCTGCCCTGTGGCTGCTCAGACCGGACGT 1266
Db 3305 GGTGCGGGGAGATTCGGGCTGATTTGCTGCCCTGTGGCTGCTCAGACCGGACGT 3364
QY 1267 GCGATGATGGATCAGGGCTCCGGGACGTGCTCTGTGAAACGGGGTGGACAGGCCCT 1326
Db 3365 GCGATGATGGATCAGGGCTCCGGGACGTGCTCTGTGAAACGGGGTGGACAGGCCCT 3424
QY 1327 CGTGTGACACTCAGGAGTTTTTCCCTGCAAGTGTGTAACGCTCTTGTTCGTGATGCCA 1386
Db 3425 CGTGTGACACTCAGGAGTTTTTCCCTGCAAGTGTGTAACGCTCTTGTTCGTGATGCCA 3484
QY 1387 CCTGTGAAGAGAACACACGTGTGAGTGTAACTGTGATTTATGAGTGTGAGGATCAGAT 1446
Db 3485 CCTGTGAAGAGAACACACGTGTGAGTGTAACTGTGATTTATGAGTGTGAGGATCAGAT 3544
QY 1447 GCACATCTGTGATTTCTCAAAACAGGACAAACGGGGCTGTGCAAAAGGTGGCCAGATGCT 1506
Db 3545 GCACATCTGTGATTTCTCAAAACAGGACAAACGGGGCTGTGCAAAAGGTGGCCAGATGCT 3604
QY 1507 CCCAGAGGGCACGAGAGTCTCTGTGAGTGTGCAAGAGGATACAAAGGGGACGCGGAC 1566
Db 3605 CCCAGAGGGCACGAGAGTCTCTGTGAGTGTGCAAGAGGATACAAAGGGGACGCGGAC 3664
QY 1567 GCTGCAACAGATAGACCTTGTGACAGGGCTTAAACGGAGGGTGTACAGGACGACCA 1626

Db 3665 GCTGCACAGATAGACCCCTGTGCAGACGGCCTTAACGAGGGTGTACAGGACGCCA 3724
Qy 1627 CTTGTAAGATGACAGCCCGGGGCAAGCAAGTGTGAGTGTAAAGTCACTATGTGCGAG 1686
Db 3725 CTTGTAAGATGACAGCCCGGGGCAAGCAAGTGTGAGTGTAAAGTCACTATGTGCGAG 3784
Qy 1687 ATGGGCTGAACCTGTAGCGCGGAGCAGCTGCCATTGACCGCTGCTTACAGGACAATGGGC 1746
Db 3785 ATGGGCTGAACCTGTAGCGCGGAGCAGCTGCCATTGACCGCTGCTTACAGGACAATGGGC 3844
Qy 1747 AGTGCCATCAGACGCGCAATGTGCGACCTCCACTTTCAGGATACCACTGTGCGGTCT 1806
Db 3845 AGTGCCATCAGACGCGCAATGTGCGACCTCCACTTTCAGGATACCACTGTGCGGTCT 3904
Qy 1807 TCCATCTAGCTCCCACTGGGCGAGTATAAGCTGACCTTTGACAAAGCCAGAGGGCT 1866
Db 3905 TCCATCTAGCTCCCACTGGGCGAGTATAAGCTGACCTTTGACAAAGCCAGAGGGCT 3964
Qy 1867 GTGCCAAACGAAGCTCGACCATGGCAACCTACCAACAGCTCTCTATGCCAGAGGCCA 1926
Db 3965 GTGCCAAACGAAGCTCGACCATGGCAACCTACCAACAGCTCTCTATGCCAGAGGCCA 4024
Qy 1927 AGTACCACCTGTGCTCAGCAGGCTGGCTGGAGACGGGGGCTTGCTTACCCACAGCT 1986
Db 4025 AGTACCACCTGTGCTCAGCAGGCTGGCTGGAGACGGGGGCTTGCTTACCCACAGCT 4084
Qy 1987 TCGCTCCCAAGCTGTGGCTCTGTGTGGTGGATAGTGAACCTAGACCCCA 2046
Db 4085 TCGCTCCCAAGCTGTGGCTCTGTGTGGTGGATAGTGAACCTAGACCCCA 4144
Qy 2047 ACACAGAGTGAATGTGGGATGCTTCTGCTATCGGATGAAGATGTGAACCTGCA 2106
Db 4145 ACACAGAGTGAATGTGGGATGCTTCTGCTATCGGATGAAGATGTGAACCTGCA 4204
Qy 2107 AGTGGGCTATGTGGGAGATGCTTCTCATGCACTGGGAACTGCTGAGGCTCTGATGT 2166
Db 4205 AGTGGGCTATGTGGGAGATGCTTCTCATGCACTGGGAACTGCTGAGGCTCTGATGT 4264
Qy 2167 CTTTCCCTCTACTCAAACTTCTGACGGAAGTGTGCTGCTGCTGCTGCTGCTGCTGCT 2226
Db 4265 CTTTCCCTCTACTCAAACTTCTGACGGAAGTGTGCTGCTGCTGCTGCTGCTGCTGCT 4324
Qy 2227 GAGGCGGTGCAATTTCTAGAACCTGACTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2286
Db 4325 GAGGCGGTGCAATTTCTAGAACCTGACTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4384
Qy 2287 CACAGAACAGTGGGCTGGGAGATGAGACCTTCTGCTGGCGGAGACATCGAGCACACC 2346
Db 4385 CACAGAACAGTGGGCTGGGAGATGAGACCTTCTGCTGGCGGAGACATCGAGCACACC 4444
Qy 2347 TCGCCAATGTGAGATGTTTTTCTACAACTGCTTGTCAATGGCACCACTGCAAAAGCA 2406
Db 4445 TCGCCAATGTGAGATGTTTTTCTACAACTGCTTGTCAATGGCACCACTGCAAAAGCA 4504
Qy 2407 GGGTGGGAAGCAAGCTGCTATCATCTGCCAGCGAGACCACTTCTGCTGCTGCTGCTGCTGCT 2466
Db 4505 GGGTGGGAAGCAAGCTGCTATCATCTGCCAGCGAGACCACTTCTGCTGCTGCTGCTGCTGCT 4564
Qy 2467 GGTGTTGTGAGGAGAGCCATTTCTGAGTGGGAGATCTTTGCTGCTGCTGCTGCTGCTGCT 2526
Db 4565 GGTGTTGTGAGGAGAGCCATTTCTGAGTGGGAGATCTTTGCTGCTGCTGCTGCTGCTGCT 4624
Qy 2527 ATGTCATTTCCAGGCTTTAAAGACCCCTGCGCCCGCTGACCTTTGACCCACACTGGCT 2586
Db 4625 ATGTCATTTCCAGGCTTTAAAGACCCCTGCGCCCGCTGACCTTTGACCCACACTGGCT 4684
Qy 2587 TGGGAGCAGGATCTTCTTCCCATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2646
Db 4685 TGGGAGCAGGATCTTCTTCCCATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4744
Qy 2647 ACTCCTACTTTCCGATAAACCGGAGAACAAATCGGCTTCCAGCATTTTGGTTCGGAAGG 2706
Db 4745 ACTCCTACTTTCCGATAAACCGGAGAACAAATCGGCTTCCAGCATTTTGGTTCGGAAGG 4804

Qy 2707 ACATTAATTTGTCAGCTTTGGCAGCAGCAGCCTTCTGCAATATCTCGAACCCCTTCTATG 2766
Db 4805 ACATTAATTTGTCAGCTTTGGCAGCAGCAGCCTTCTGCAATATCTCGAACCCCTTCTATG 4864
Qy 2767 AGAGCACAACCTCAGCTCCCCCAGAACCTTCTTACGACCCCTTACGGACTCTGAAGAAC 2826
Db 4865 AGAGCACAACCTCAGCTCCCCCAGAACCTTCTTACGACCCCTTACGGACTCTGAAGAAC 4924
Qy 2827 GGCAGCTTGGAGGCAATGACCCCTTGGAGACACTGTGA 2864
Db 4925 GGCAGCTTGGAGGCAATGACCCCTTGGAGACACTGTGA 4962

RESULT 7

AAF87120

ID AAF87120 standard; DNA; 3625 BP.

XX AAF87120;

XX AAF87120;

DT 26-MAR-2002 (first entry)

XX NOV9 coding sequence.

XX NOV; Cytostatic; contraceptive; antiinflammatory; immunomodulatory;
cardiovascular; casein kinase II phosphorylation site; contraception;
serine/threonine kinase; Peutz-Jeghers syndrome; cellular proliferation;
epidermal growth factor; cell development; apoptosis; cell adhesion;
growth migration; cell structure; motility; cancer; immune disorder;
inflammatory disorder; cellular adhesion disorder; long-QT syndrome;
cardiovascular disease; hypertrophic cardiomyopathy; marfan syndrome;
therapy; NOV1; NOV2; NOV3; NOV4; NOV5; NOV6; NOV7; NOV8; NOV9; NOV10;
NOV11; NOV12; NOV13; NOV14; NOV15; NOV16; NOV17; NOV18; NOV19; NOV20;

XX Unidentified.

XX Key Location/Qualifiers

CDS 387..2024

FT /*tag= a

FT /product= "NOV9"

XX WO200036638-A2.

XX 25-MAY-2001.

XX 17-NOV-2000; 2000WO-US031543.

XX 19-NOV-1999; 99US-0166336P.

XX 29-NOV-1999; 99US-0167785P.

XX 08-MAR-2000; 2000US-0187844P.

XX 16-NOV-2000; 2000US-00715417.

XX (CURA-) CURAGEN CORP.

XX Shimkets RA, Lichenstein H, Vernet C, Fernandes E;

XX WPI; 2001-648134/74.

XX P-PSDB; AAB83365.

XX Novel human polypeptides and the nucleic acids that encode them useful
for preventing, diagnosing and treating e.g. cancer, inflammation and
immune disorders.

XX Claim 9; Page 32-33; 141pp; English.

XX This sequence encodes the NOV9 protein. The invention relates to the NOV1
-NOV16 proteins, and their coding sequences. The proteins have Cytostatic
; contraceptive; antiinflammatory; immunomodulatory; and cardiovascular
activities. The sequences may be used in the prevention, diagnosis and
treatment of diseases associated with inappropriate NOVX expression. They
may be used to treat disorders associated with decreased expression by
rectifying mutations or deletions in a patient's genome that affect the
activity of protein by expressing inactive proteins or to supplement the

CC patients own production of protein. They are used to produce NOVX
CC proteins, by inserting the nucleic acid into a cell and culturing it to
CC express the protein. The DNA may be used as DNA probes in assays to
CC detect and quantitate the presence of similar DNAs in samples, and which
CC patients may need restorative therapy. The NOVX protein may also be used
CC as antigens in the production of antibodies (Abs) against NOVX and in
CC assays to identify modulators of NOVX expression and activity. The anti-
CC NOVX Abs and antagonist are used to down regulate expression and
CC activity. The anti-NOVX Abs are used for detecting the presence of NOVX
CC in samples. Disorders that may be prevented, diagnosed and/or treated
CC vary depending on the NOVX protein. NOV1, NOV3, NOV5, NOV7, NOV9-11 and
CC NOV13-16 have casein kinase II phosphorylation sites characteristic of
CC serine/threonine kinases, and are used to treat kinase-related disorders
CC (e.g. Peutz-Jeghers syndrome, cellular proliferation and contraception).
CC NOV2-3, NOV6 and NOV8 are homologous to the epidermal growth factor (EGF)
CC -like super family and are involved in, e.g. regulation of cell
CC development, apoptosis, cell adhesion, growth migration, cell structure
CC and motility and protein management, and are used to treat cancers,
CC inflammatory disorders, immune disorders and cellular adhesion disorders.
CC NOV6-10 are homologous to EGF-like fibrillin proteins and are used to
CC treat cardiovascular disease e.g. hypertrophic cardiomyopathy, long-QT
CC syndrome and marfan syndrome
XX
SQ Sequence 3625 BP; 896 A; 971 C; 914 G; 844 T; 0 U; 0 Other;

Query Match 86.8%; Score 2828.8; DB 4; Length 3625;
Best Local Similarity 95.1%; Pred. No. 0;
Matches 2985; Conservative 0; Mismatches 43; Indels 111; Gaps 2;
QY 122 AGCCTTTGATGAGGAAGCTCGGTTAAAGACTGGGACAAATACGGTTTAAATGCCCCAGGT 181
DB 569 ACCCTCTGATCTCTGTTACAGGTTAAAGACTGGGACAAATACGGTTTAAATGCCCCAGGT 628
QY 182 TCTTCGGTACCATGTGGTCCGCTGCCACCAAGCTGCTCTTGGAACAACTGAAATTTGATCTC 241
DB 629 TCTTCGGTACCATGTGGTCCGCTGCCACCAAGCTGCTCTTGGAACAACTGAAATTTGATCTC 688
QY 242 AAATGCTACTTCCCTCAAGGAGAGCCATAGTATCATCTCCGCTCTCAGAGCAGCGTGA 301
DB 689 AAATGCTACTTCCCTCAAGGAGAGCCATAGTATCATCTCCGCTCTCAGAGCAGCGTGA 748
QY 302 TATAAATAAAGGCTAAGATCATATCCAGTGTATCATCAGTACTAATGGGATTTGTTCA 361
DB 749 TATAAATAAAGGCTAAGATCATATCCAGTGTATCATCAGTACTAATGGGATTTGTTCA 808
QY 362 TATCATAGCAAAATGCTATCTCCCAAAATTTGCTTTATCATCTCCCAAGACAACTCTGG 421
DB 809 TATCATAGCAAAATGCTATCTCCCAAAATTTGCTTTATCATCTCCCAAGACAACTCTGG 868
QY 422 AAGAATCTGCAAAATCTTACGACTTTGGCAACAACAAATGGCTTACATCAAAATTTAGCAA 481
DB 869 AAGAATCTGCAAAATCTTACGACTTTGGCAACAACAAATGGCTTACATCAAAATTTAGCAA 928
QY 482 CTTTAATACAGGACTCAGGTTTGTGAGTGTATCATCCCGATCCCATCCACACCCCAAGTCA 541
DB 929 CTTTAATACAGGACTCAGGTTTGTGAGTGTATCATCCCGATCCCATCCACACCCCAAGTCA 988
QY 542 TCTCTCTTGCCCAACGACCAAGCCCTCCATGCGCTTACCTGCTGGAACAACAGGACTTCT 601
DB 989 TCTCTCTTGCCCAACGACCAAGCCCTCCATGCGCTTACCTGCTGGAACAACAGGACTTCT 1048
QY 602 GTTCAACCAAGACAACAGGACAAGCTGAAGGAGTATTTCAAGTTTTCATGTGATACGAGA 661
DB 1049 GTTCAACCAAGACAACAGGACAAGCTGAAGGAGTATTTCAAGTTTTCATGTGATACGAGA 1108
QY 662 TGCCAAAGTTTATGCTGTGATCTTCCCAATCCATGCTGCTGGAAGACCCCTGCAAGGTTTC 721
DB 1109 TGCCAAAGTTTATGCTGTGATCTTCCCAATCCATGCTGCTGGAAGACCCCTGCAAGGTTTC 1168
QY 722 AGAGCTGAGTGTGAATGTGAGCTGGCAGGACATCGGTGACCTCTTTCTGATGACCA 781
DB 1169 AGAGCTGAGTGTGAATGTGAGCTGGCAGGACATCGGTGACCTCTTTCTGATGACCA 1228

QY 782 AACCTGCAGAAATGTGTCAGCGGAGAGCTCTTTGTTGACCTGGTGTGGCTACGGCAATGA 841
DB 1229 AACCTGCAGAAATGTGTCAGCGGAGAGCTCTTTGTTGACCTGGTGTGGCTACGGCAATGA 1288
QY 842 CTGCTCTGATGATTTCCACCCCTGGGGGGCGGTGTGACACCTTTACTCTTTTCGATGC 901
DB 1289 CTGCTCTGATGATTTCCACCCCTGGGGGGCGGTGTGACACCTTTACTCTTTTCGATGC 1348
QY 902 CTCGGGGCAGTGTGGAGCTGTGTCAATCTCCAGCTGCCCAAGGTGGAGTAACCCAAA 961
DB 1349 CTCGGGGCAGTGTGGAGCTGTGTCAATCTCCAGCTGCCCAAGGTGGAGTAACCCAAA 1408
QY 962 GGGTCTGAAGCAGAAAGTGTCTCTACAACCTGCCCTTCAAGAGAACTTGAAGGCTGCCG 1021
DB 1409 GGGTCTGAAGCAGAAAGTGTCTCTACAACCTGCCCTTCAAGAGAACTTGAAGGCTGCCG 1468
QY 1022 GGAGCGGTGCAGCCTGGTGTATCAGATCCCAGGTGCTGCAAGGGCTACTTCGGGGGAGA 1081
DB 1469 GGAGCGGTGCAGCCTGGTGTATCAGATCCCAGGTGCTGCAAGGGCTACTTCGGGGGAGA 1528
QY 1082 CTGTGAGGCTGCCCTGCGAGGAGACAGATGCCCCCTGTATTAACCGGGGTGTCTGCCCTGA 1141
DB 1529 CTGTGAG---GGTGGGGTGCCTCTTCCCCCTCGCAACTCTAAAAGTGTCTGCCCTGA 1584
QY 1142 TCAGTACTCGGCCACCGGAGAGTGTAAATGCAACACCGGCTTCAATGGGACCGGCTGTA 1201
DB 1585 TCAGTACTCGGCCACCGGAGAGTGTAAATGCAACACCGGCTTCAATGGGACCGGCTGTA 1644
QY 1202 GATGTGCTGGCCGGGGAGATTCGGGCCCTGATTTGCTGCCCTGTGGCTCTCAGACCAACCG 1261
DB 1645 GATGTGCTGGCCGGGGAGATTTGGGCCCTGATTTGCTGCCCTGTGGCTGTCTCAGACCAACCG 1704
QY 1262 ACAGTGCAGATGATGGCATCACGGGCTCCGGGCGAGTGCCTCTGTGAAAACGGGGTGGACAG 1321
DB 1705 ACAGTGCAGATGATGGCATCACGGGCTCCGGGCGAGTGCCTCTGTGAAAACGGGGTGGACAG 1764
QY 1322 CCCCTGCTGTGACACTCAGCGAGTGTTCCTGCGAGTGTAGCCCTCTTTGTTCTGCTCA 1381
DB 1765 CCCCTGCTGTGACACTCAGCGAGTGTTCCTGCGAGTGTAGCCCTCTTTGTTCTGCTCA 1824
QY 1382 TGGCACTGTAAAGGAGAAACAACGCTGTGAGTGTAACTGGATTAAGAGGTGACCGAAT 1441
DB 1825 TGGCACTGTAAAGGAGAAACAACGCTGTGAGTGTAACTGGATTAAGAGGTGACCGAAT 1884
QY 1442 CACATGCACAGTTGTGGATTTCTGCAACAGGACAAACGGGGGCTGTGCAAAAGGTGGCCAG 1501
DB 1885 CACATGCACAGTTGTGGATTTCTGCAACAGGACAAACGGGGGCTGTGCAAAAGGTGGCCAG 1944
QY 1502 ATGCTCCCAAGAGGGCAACGAGGTCTCTGCGAGCTGCCAGAGGGGATACAAAGGGGACGG 1561
DB 1945 ATGCTCCCAAGAGGGCAACGAGGTCTCTGCGAGCTGCCAGAGGGGATACAAAGGGGACGG 2004
QY 1562 GCACAGCTGCACAGATAGACCCCTGTGCGAGCGGCTTAAACGAGGGGTGTCCACGAGCA 1621
DB 2005 GCACAGCTGCACAGATAGACCCCTGTGCGAGCGGCTTAAACGAGGGGTGTCCACGAGCA 2064
QY 1622 CGCCACTGTAAAGATCACAGGCGCGGGCAAGCAACAAGTGTGAGTGTAAAGTCACTATGT 1681
DB 2065 CGCCACTGTAAAGATCACAGGCGCGGGCAAGCAACAAGTGTGAGTGTAAAGTCACTATGT 2124
QY 1682 CGGAGATGGGCTGAACCTGTGAGCGGAGAGCTGCCCATTTGACCGCTGTACAGGACAA 1741
DB 2125 CGGAGATGGGCTGAACCTGTGAGCGGAGAGCTGCCCATTTGACCGCTGTACAGGACAA 2184
QY 1742 TGGGAGTGCATGTCAGACGCAAAATGTGTGCACTCCACTTCCAGGATACCACTGTGG 1801
DB 2185 TGGGAGTGCATGTCAGACGCAAAATGTGTGCACTCCACTTCCAGGATACCACTGTGG 2244
QY 1802 GGTGTTCCATCTACGCTCCCACTGGGCGAGTAAAGTGAACCTTTGACAAAGCCAGAGA 1861
DB 2245 GGTGTTCCATCTACGCTCCCACTGGGCGAGTAAAGTGAACCTTTGACAAAGCCAGAGA 2304
QY 1862 GGCTGTGCCAACGAGAGCTGGACCATGGCAACCTACACACAGCTCTCTCTATGCCAGAA 1921

Db 2305 GGCCTGTGCAACGAAGCTGGACCATGCAACCTACACCAAGCTCTCTATGCCAGAA 2364
QY 1922 GGCCAAAGTACCCTGTGTCTGACAGGCTGGTGGAGACCGGGCGGGTTGCCCTACCCAC 1981
Db 2365 GGCCAAAGTACCCTGTGTCTGACAGGCTGGTGGAGACCGGGCGGGTTGCCCTACCCAC 2424
QY 1982 AGCCTTCGCTCCCAAGACTGTGGCTCTGGTGGTGGAGTAGTGACATATGGACCTAG 2041
Db 2425 AGCCTTCGCTCCCAAGACTGTGGCTCTGGTGGTGGAGTAGTGACATATGGACCTAG 2484
QY 2042 ACCCAACAAGAGTGAATATGGGATGTCTTCTGCTATCGGATGAAAGATGTGAATGCGAC 2101
Db 2485 ACCCAACAAGAGTGAATATGGGATGTCTTCTGCTATCGGATGAA 2530
QY 2102 CTGCAAGGTGGGCTATGTGGGAGATGGCTTCTCATGCACTGGGAACCTGCTGAGTCT 2161
Db 2531 ----- 2530
QY 2162 GATGTCTTCCCTCACTCACAAACTTCTGAGGAGTGTCTGCTCATCGGACCTTATCCAAAGCTC 2221
Db 2531 -----GGAAGTGTGGCTATTTCCAAAGCTC 2557
QY 2222 AGCTCAGGCGCTGCAATTTCTAGAACACCTGACTGACCTGTCTCATCCGCGGACCTCTT 2281
Db 2558 AGCTCAGGCGCTGCAATTTCTAGAACACCTGACTGACCTGTCTCATCCGCGGACCTCTT 2617
QY 2282 TGTGCCACAGAACAGTGGGCTGGGGGAGATGAGACCTTGTCTGGCGGGACATCGAGCA 2341
Db 2618 TGTGCCACAGAACAGTGGGCTGGGGGAGATGAGACCTTGTCTGGCGGGACATCGAGCA 2677
QY 2342 CCACCTCCCAATGTGACATGCTTTTCTACAACTGCTGCAATGACCTTGTCAATGGACACCTTGA 2401
Db 2678 CCACCTCCCAATGTGACATGCTTTTCTACAACTGCTGCAATGACCTTGTCAATGGACACCTTGA 2737
QY 2402 AACGAGGTGGGAAGCAAGCTGCTCATCACTGCCAGCAGGACCACTCCAAACCCAGCA 2461
Db 2738 AACGAGGTGGGAAGCAAGCTGCTCATCACTGCCAGCAGGACCACTCCAAACCCAGCA 2797
QY 2462 GACCAAGTTTGTGTAGTAAGAGCAATCTGTGAGTGGGACATCTTTGCTCCAAATGGAT 2521
Db 2798 GACCAAGTTTGTGTAGTAAGAGCAATCTGTGAGTGGGACATCTTTGCTCCAAATGGAT 2857
QY 2522 CATTCATGCTCATTTCCAGGCTTTAAAGACCCCTGCGCCGCGGACCTTGAACCCAC 2581
Db 2858 CATTCATGCTCATTTCCAGGCTTTAAAGACCCCTGCGCCGCGGACCTTGAACCCAC 2917
QY 2582 TGGCTTGGGAGCAGGATCTTCTTTGCCATCATCTGTGTGACTGGGGCTGTGCTTGGC 2641
Db 2918 TGGCTTGGGAGCAGGATCTTCTTTGCCATCATCTGTGTGACTGGGGCTGTGCTTGGC 2977
QY 2642 TGCTTACTCTTACTTGGATTAACCGGAGAACATCGGCTTCCAGCAATTTGAGTGGGA 2701
Db 2978 TGCTTACTCTTACTTGGATTAACCGGAGAACATCGGCTTCCAGCAATTTGAGTGGGA 3037
QY 2702 AGAGCAATTAATGTGACGCTCTTGGCAAGCAGCAGCTGAGATATCTCGAACCCCTT 2761
Db 3038 AGAGCAATTAATGTGACGCTCTTGGCAAGCAGCAGCTGAGATATCTCGAACCCCTT 3097
QY 2762 GTATGAGAGCAACCTCAGCTCCCGCAGAACCTTCTTACGACCCCTTACGGACTCTGA 2821
Db 3098 GTATGAGAGCAACCTCAGCTCCCGCAGAACCTTCTTACGACCCCTTACGGACTCTGA 3157
QY 2822 AGAAGCGAGCTTGAAGGCAATGACCTTGGAGACACTGTGAGGCGCTGGACGGAGAT 2881
Db 3158 AGAAGCGAGCTTGAAGGCAATGACCTTGGAGACACTGTGAGGCGCTGGACGGAGAT 3217
QY 2882 GCCAGGCACTCACTCACTGCCACCTGGGCACTCACTGTGAATCTCAGCACCAGTTGGCT 2941
Db 3218 GCCAGGCACTCACTCACTGCCACCTGGGCACTCACTGTGAATCTCAGCACCAGTTGGCT 3277
QY 2942 TTTAGGAACGTAAAGTCTTTTAAAGCACTCAGAAGCCATCACTCTCTCTGGCTGATCT 3001

Db 3278 TTTAGGAACGTAAAGTCTTTTAAAGCACTCAGAAGCCATACCTCATCTCTCTGGCTGATCT 3337
QY 3002 GGGGGTGTGTTTCTGTGGGTGAGAGATGTGTTGCTGTGCCCCACCCAGTACAGCTTCTCTCT 3061
Db 3338 GGGGGTGTGTTTCTGTGGGTGAGAGATGTGTTGCTGTGCCCCACCCAGTACAGCTTCTCTCT 3397
QY 3062 CTGACCCCTTGGCTCTTCTTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 3121
Db 3398 CTGACCCCTTGGCTCTTCTTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 3457
QY 3122 ACATCATGCGTAACTGTGATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 3181
Db 3458 ACATCATGCGTAACTGTGATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 3517
QY 3182 CCAGGCCCTTAGCCAGTGTCTGACACAGGAACCTGTGCAAAATAAAGGTTTATGGACAGA 3241
Db 3518 CCAGGCCCTTAGCCAGTGTCTGACACAGGAACCTGTGCAAAATAAAGGTTTATGGACAGA 3577
QY 3242 AAAAAAATAAAGGTTTATGGACAGA 3260
Db 3578 AACAAAGTCAAAAAAATAAAGGTTTATGGACAGA 3596

RESULT 8

ABA04648

ID ABA04648 standard; cDNA; 4706 BP.

XX ABA04648;

XX AC (first entry)

XX 22-FEB-2002 (first entry)

XX Rat Hyaluronic Acid Receptor for Endocytosis, HARE, coding sequence.

DE HARE; Hyaluronic Acid Receptor for Endocytosis; hyaluronan; chondroitin;

KW chondroitin sulphate; extracellular matrix; cartilage; skin;

KW vitreous humour; endocytic receptor; glycosaminoglycan; rat; ss.

XX Rattus norvegicus.

XX Key Location/Qualifiers

FH 1.4296

FT /tag= a

FT /partial

FT /product= "Rat HARE"

FT /note= "No start codon given"

PN W0200181544-A2.

PD 01-NOV-2001.

XX 25-APR-2001; 2001WO-US013403.

XX 25-APR-2000; 2000US-0199538P.

PR 02-NOV-2000; 2000US-0245320P.

XX (WEIG// WEIGEL P A.

PA (ZHOU// ZHOU B.

PA (WEIG// WEIGEL J A.

XX Weigel PA, Zhou B, Weigel JA;

XX WPI; 2002-049271/06.

DR P-PSDB; AAM47675.

XX New mammalian hyaluronic acid receptor for endocytosis, useful e.g. for

XX identifying agents that inhibit binding to hyaluronic acid, and related

XX nucleic acid.

PS Claim 49; Fig 21; 263pp; English.

XX The present invention relates to sequences for rat and human HARE

CC (Hyaluronic Acid Receptor for Endocytosis, ABA04648, ABA04662, AAM47675

CC and AAM47684). HARE can bind specifically to at least one of hyaluronic

QY	11	GGAGCTTCCCAAGAAACCGGAAACCTTCCAGATATTTCTTCAGTTGCGAGGACATTTGCT	70
Db	1395	GGAGCTTCCCAAGAAACCGGAAACCTTCCAGATATTTCTTCAGTTGCGAGGACATTTGCT	1454
QY	71	GAAGATCTGTCGGCGCGCCAGCGCCCTTCACTGTTTTCGACCTTTATCTGCGAGCTTTGA	130
Db	1455	CCGAGAGCTTGTGACCTGGCCCTTCACTGTTTTCGCGCTTTGTCTAGCTCTTTCAA	1514
QY	131	TGAGGAAGCTCGGGTTAAAGAATGGGACAAATACCGTTTAAATGCCCGGCTTTTCGGTA	190
Db	1515	TCATGAGCCCGGATTAAGACTGGGATCAGCAGGCGCTCAATGCCAGGTTTTCGGTA	1574
QY	191	CCATGTCGCTGCGCACAGCTGTTCTGGAACCTGGAATTAATGATCTCAATGCTAC	250
Db	1575	TCACCTGGTGGCTGCCAGCAGCTGCTGTGGACAACTTAAAGTGACCAAGTGCCAC	1634
QY	251	TTCCCTCCAGAGAGGCAATAGTATCTCCGCTCTTCAGACACGGTGTATATAATAA	310
Db	1635	GACCTCCAGAGAGGCGAGTTTCCATCTCTCTCTCAGGACATGCTTCTATTAACNA	1694
QY	311	TAAAGCTAAGATCATATCCAGTGATATCATAGTACTAATGGGATTTTCATATCATAGA	370
Db	1695	TGAGGCGAGGTCCTGTCAGTGACATCATCAGCACCAATGGCTCATCCAGTTATAGA	1754
QY	371	CAAAATGCTATCTCCCAAAATTTGCTTATCATCTCCCAAGACAACTCTGGAGATTTCT	430
Db	1755	CAAATGCTGCTCTCCCAAAATCTTGTATATACCCCAAGATGCTTGGCGAGGTTCT	1814
QY	431	GCAAAATCTTACGACTTTCGCAACAAATGCTACTACAAATTTAGCAACTTAATACA	490
Db	1815	GCAAAATCTTACTACAGTGAGCAACCAACGATATACCAATTCAGCAAGTTGATACA	1874
QY	491	GGACTCAGGTTTGTGAGTGTCATCACCGATCCCATCCACACCCAGTCACTCTCTCTG	550
Db	1875	GGACTCAGGTTTGTGAGTGTCATCACCGATCCCATCCACACCCAGTCACTCTCTCTG	1934
QY	551	GCCACCGAGCAAGCCCTCATGCCCTAATCTGCTGAACACAGGACTTCTGTTCAACCA	610
Db	1935	GCCTACGCAACAAAGCCCTGGAAGCCCTGCCCCAGAGCAGCAGGACTTCTGTTCAATCA	1994
QY	611	AGACAAACAGGCAAGCTGAAGGATTTGAAGTTTCAATGATACGAGATGCCAAGGT	670
Db	1995	AGACAAACAGGCAAGCTGAAGGATTTGAAGTTTCAATGATACGAGATGCCAAGGT	2054
QY	671	TTTAGCTGTGATCTTCCACATCCACTGCTCGAAGACCTCGAAGTTTCAGAGCTGAG	730
Db	2055	TTTAGCTTCAGACTTCCCAAGTCTGCTTCCCTGGAAGACCTTGAAGGCTCAGAGCTGAG	2114
QY	731	TGTGAATGTGGAGCTGGCAGGACATCGGTGACCTTTCTGAATGGCCCAACCTGCAG	790
Db	2115	TGTGAGGTGTGAACTGGCAGTGACATCGGTGAGCTCTTCTTAAACGAAATATGTCAG	2174
QY	791	AATTTGTGACGGGAGCTCTTTGTTGACCTGGGTGTGGCTACGGCAATGACTGTCTGCT	850
Db	2175	ATTCTACACGGGGACTCTTTGTTGAGCTGGGTGTGGCTATGACATGACCTGCTACT	2234
QY	851	GATTTGATCCCACTGGGGGGCGCTGTGACACCTTTTACTTTTCACTTTGATCCCTGGGGA	910
Db	2235	CATGAATCTTACCTAGGTGGCGGATGTGACACTTTTACTTTTACCTTTGATATTCGGGGGA	2294
QY	911	GTGTGGAGCTGTGTAATCTCCAGCTCCCAAGGTGGATTAACCAAGGTTGTGAA	970
Db	2295	GTGCGGAAGTTGCAATTTTCACTCCCAATGCCACTGAAGAGCAAGCAAGGGGCTGAA	2354
QY	971	GCAAGTGTCTCTACAACCTTTCGCTTCAAGAGGAACTGGAAGGCTGCGGGAGCG	1027
Db	2355	GAAGAAGTGTATCTACAACCTGTTACCTTTTACAGAGGAACTGGAAGGCTGCCAAGCT	2414
QY	1028	GTGAGCCTGTGTATACAGATCCCAAGGTGTGCAAGGCTACTTTCGGGGAGACTGTCA	1087
Db	2415	GTGACCGTGTGTATCCAAACCCCGAGTGTGCTGCTGCTTACTTTCATGCGAGCTGTCA	2474
QY	1088	GGCTTCCCTCGAGGACCAAGATGCCCTGTATAAACCGGGTGTCTCCTTGTATCATGTA	1147
Db	2475	GGCTTCCCTCGAGGACCAAGATACACCTGTATAAACCGGGCATGTGCGCGATCTGTA	2534
QY	1148	CTCGGCCACCGGAGAGTGTAAATGCAACACCGGCTTCAATGGGACGGGTGTGAGATGTG	1207
Db	2535	CACACCCATGGGACAGTGCCTATGCAACACCGGCTTCAACGGGACAGCTGCGAGCTCTG	2594
QY	1208	CTGGCCGGGAGATTTGGGGCTGATTTGCTGCTCTGCTGCTCAGACCAACCGGACAGTG	1267
Db	2595	CTGGCATGGGAGATTTGGGGCTGATTTGCTGCTCTGCTGCTCAGACCAACCGGACAGTG	2654
QY	1268	CGATGATGGCATTCAGGGCTCCGGGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1327
Db	2655	TGATGAGGGATTCAGGCTCCGGGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	2714
QY	1328	GTGTGACATCTCAGGAGTTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1387
Db	2715	GTGTGACATCTCAGGAGTTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	2774
QY	1398	CTGTAAGGAGAACACACCTGTGAGTGTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1447
Db	2775	CTGTAAGGAGAACACACCTGTGAGTGTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	2834
QY	1448	CACAGTTGTGGATTTCTGCAACACAGGACCAACCGGGCTGTGCAAAAGGTGGCCAGATGCTC	1507
Db	2835	CACAGTTGTGGATTTCTGCAACACAGGACCAACCGGGCTGTGCAAAAGGTGGCCAGATGCTC	2894
QY	1508	CCAGAAAGGACGAAAGGTTCTCTGAGCTGCCAGAGGATACAAAGGGAGCGGCACAG	1567
Db	2895	CCAGAAAGGACGAAAGGTTCTCTGAGCTGCCAGAGGATACAAAGGGAGCGGCACAG	2954
QY	1568	CTGCAACAGATAGACCCCTGTGCAAGCGCTTAAACGGAGGCTGTGCAAGCACGCCAC	1627
Db	2955	CTGCAACAGATAGACCCCTGTGCAAGCGCTTAAACGGAGGCTGTGCAAGCACGCCAC	3014
QY	1628	CTGTAAGATGACAGGCGCCGGGCAAGCAAGTGTGAGTGTAAAGTCACTATGTGCGAGA	1687
Db	3015	CTGCAAGATGACAGGCGCCGGGCAAGCAAGTGTGAGTGTAAAGTCACTATGTGCGAGA	3074
QY	1688	TGGGCTGAATCTGAGCGCGGAGCTGCCATTTGACCGCTGCTTACAGGACAAATGGGCA	1747
Db	3075	CGAGTGTGACTGTGAGCTGTGAGCTGCCCTGCGCCCTGCGCCCTGCTTACAGCAACCGGACA	3134
QY	1748	GTGCCATGACAGCGCAAAATGTGCAACCTTCCACTTCCAGGATACCACTTGTGGGGTGT	1807
Db	3135	GTGCCATGACAGCGCAAAATGTGCAACCTTCCACTTCCAGGATACCACTTGTGGGGTGT	3194
QY	1808	CCATCTACCTCCTCCACTGGGCGAGTATTAAGCTGACCTTTGACAAAGGACAGAGGCTG	1867
Db	3195	CCATCTACCTCCTCCACTGGGCGAGTATTAAGCTGACCTTTGACAAAGGACAGAGGCTG	3254
QY	1868	TGCAACGAGAGCTGCCAGCATGCAACCTTACACCACTTCCCTATGCCCCAGAGGCA	1927
Db	3255	TGCAACGAGAGCTGCCAGCATGCAACCTTACACCACTTCCCTATGCCCCAGAGGCA	3314
QY	1928	GTACCACTCTGTCTCAGCAGGCTGGCTGGAGACCGGGCGGGTTCCTTACCCCAAGCCTT	1987
Db	3315	GTATACCTCTGTCTCAGCAGGCTGGCTGGAGAGTGGGCGGGTTCCTTACCCCAAGCCTT	3374
QY	1988	CGCTTCCCAAGAACTGTGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	2047
Db	3375	TGCTTCTCAGAAAGTGTGGTGCACAACTGTTGGGATCTGAGACTTACCGATCCAGGGGCA	3434
QY	2048	CAGAGTGAATCTGGGAGTCTTCTGCTATCGATGAAAGATGTGAACCTGCACTGCA	2107
Db	3435	CAGAGTGAATCTGGGAGTCTTCTGCTATCGATGAAAGATGTGAACCTGCACTGCA	3494
QY	2108	GGTGGGCTATGTGGGAGTGGCTTCTCATCAGTGGGAACTGCTGCTGCTGCTGCTGCTGCTGCT	2167
Db	3495	GGCAGGCTATGTGGGAGTGGCTTCTCATCAGTGGGAACTGCTGCTGCTGCTGCTGCTGCTGCT	3554
QY	2168	CTTCCCTCTCACTCACAACCTTCTGAGCGGAGTGTCTGCTGCTTATTTCCACAGCTCAGCTCG	2227

Db 3555 CTTCCCTCGCTCACAACCTCTCTGACAGAGTCTGGCTTTTCCAGAGCTCAGCCCG 3614
QY 2228 AGCCCGTGCATTTCTAGAACACCTGACCTGCTGTCATCGCGGACACCTCTTTGTGCG 2287
Db 3615 AGACAGGCAATTTTGAACACCTGACCTGCTGTCATCGTGGACCTGTTGTGCG 3674
QY 2288 ACAGAACAGTGGCTGGGGAGATGACCTGCTGCTGGGGGAGATCAGACACCACT 2347
Db 3675 ACAGAACAGTGGCTGGGGAGATGACCTGCTGCTGGGGGAGATCAGACACCACT 3734
QY 2348 CGCAATGTCAGCATGTTTTTCTACATGACCTTTGTCAATGGCACACCTCTGCAAGGAG 2407
Db 3735 CACTAATGTCACGCTCTCTCTTTTACAATGACCTTTGTCAATGGTACCTTTCTGAGGACTAT 3794
QY 2408 GGTGGGAGCAAGCTGCTCATCTGTCAGGACAGGACCCCACTCAACCGGACGAGACCCAG 2467
Db 3795 GCTGGGAAGCCAACTGCTCATTAACCTTCAGCCAGGACCACTCCACC---AGAGAGACCCAG 3851
QY 2468 GTTGTGTGATGGAAGAGCAATCTGACAGTGGGACATCTTTGCTCTCAATGGGATCATTTCA 2527
Db 3852 GTTGTGTGATGGAAGATCAATCTGAGTGGGACATCTGCTGGGACCAATGGGATCATTTCA 2527
QY 2528 TGTCAATTTCCAGGCTTTTAAAGCACCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2587
Db 3912 TATTAATTTCTGAACCTTTGAGAGCTCTCTCCACGGGACGCAACGGCTGCTGCTGCTGCT 3971
QY 2588 GGGAGCAGGAGTCTTTTGGCATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2647
Db 3972 GGGGACAGGTATATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4031
QY 2648 CTCCTACTTTCCGATAAAGCGGAGAACATCGGCTTCCAGCATTTTGTGCTGCGAGAGA 2707
Db 4032 CTCCTACTTTCCGCTTAAAGCAGGACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4090
QY 2708 CATTAATGTTGAGCTTTTGGCAAGCAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2767
Db 4091 CATTAATGTTGAGCTTTTGGCAAGCAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4150
QY 2768 GAGCACAACCTGAGCTTCCCGGAGAACCTTCTTACGACCCCTTTCAGGACTCTGAGAAAG 2827
Db 4151 GACCTCAGCGCGCGGACCCCGGAGAACCTTCTTACGACCCCTTTCAGGACTCTGAGAAAG 4210
QY 2828 GCAGCTTCCAGGCAATGACCCCTTCCAGGACACTGTCAGGCTGTCAGGAGATCCGAGC 2887
Db 4211 GGATCTGAGACAGCAGCCCTCTCTGGGGGCACTG---CGGTCTGACATGAGAGCCAGC 4267
QY 2888 CATCACTCACTGCCACCTGGGCGCATCACTGTGAATTTCTCAGC---ACGAGTTGCTTTT 2944
Db 4268 AAGCAACACAGTCACGGTTCCAGGTAATTCAGGCTGCTGCTGCTGCTGCTGCTGCTGCT 4327
QY 2945 AGGAACGTAAGTCTTTAAGCAGTCAGAGCCATACCTGCTGCTGCTGCTGCTGCTGCTGCT 3004
Db 4328 GTTTTAAAGATGACAACTATAGCAGCAGCCATACCTGCTGCTGCTGCTGCTGCTGCTGCT 4387
QY 3005 GGTGTTTCTGCTGGGTGAGAGATGTTG-CTGTGCGCCACCCAGTACAGCTTCTCTCTCT 3063
Db 4388 ATTGTCGCCAGGCTAAGAGCCATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4447
QY 3064 GACCTTTT 3071
Db 4448 GAGCCTAT 4455

RESULT 10
AAF87119
ID AAF87119 standard; DNA; 2483 BP.
XX
AC AAF87119;
XX
DT 26-MAR-2002 (first entry)
XX
DE NOV8 coding sequence.

XX NOV; Cytostatic; contraceptive; antiinflammatory; immunomodulatory;
KW cardiovascular; casein kinase II phosphorylation site; contraception;
KW serine/threonine kinase; Peutz-Jeghers syndrome; cellular proliferation;
KW epidermal growth factor; cell development; apoptosis; cell adhesion;
KW inflammatory disorder; cell structure; motility; cancer; immune disorder;
KW cardiovascular disease; hypertrophic cardiomyopathy; long-QT syndrome;
KW therapy; NOV1; NOV2; NOV3; NOV4; NOV5; NOV6; NOV7; NOV8; NOV9; NOV10;
KW NOV11; NOV12; NOV13; NOV14; NOV15; NOV16; ds.
XX Unidentified.
OS
XX
FH
FT Key Location/Qualifiers
FT CDS 387..2396
FT /*tag= a
FT /product= "NOV8"
XX
PN W0200136638-A2.
XX
PD 25-MAY-2001.
XX
PF 17-NOV-2000; 2000WO-US031543.
XX
PR 19-NOV-1999; 99US-0166336P.
PR 29-NOV-1999; 99US-0167785P.
PR 08-MAR-2000; 2000US-0187844P.
PR 16-NOV-2000; 2000US-00715417.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shinkets RA, Lichenstein H, Vernet C, Fernandes E;
XX WPI: 2001-648134/74.
XX P-PSDB; AAB833564.
XX
PT Novel human polypeptides and the nucleic acids that encode them useful
PT for preventing, diagnosing and treating e.g. cancer, inflammation and
PT immune disorders.
XX
PS Claim 9; Page 29-30; 141pp; English.
XX
CC This sequence encodes the NOV8 protein. The invention relates to the NOV1
CC -NOV16 proteins, and their coding sequences. The proteins have Cytostatic
CC ; contraceptive; antiinflammatory; immunomodulatory; and cardiovascular
CC activities. The sequences may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate NOVX expression. They
CC may be used to treat disorders associated with decreased expression by
CC rectifying mutations or deletions in a patient's genome that affect the
CC activity of protein by expressing inactive proteins or to supplement the
CC patients own production of protein. They are used to produce NOVX
CC proteins, by inserting the nucleic acid into a cell and culturing it to
CC express the protein. The DNA may be used as DNA probes in assays to
CC detect and quantitate the presence of similar DNAs in samples, and which
CC patients may need restorative therapy. The NOVX protein may also be used
CC as antigens in the production of antibodies (Abs) against NOVX and in
CC assays to identify modulators of NOVX expression and activity. The anti-
CC NOVX Abs and antagonist are used to down regulate expression and
CC activity. The anti-NOVX Abs are used for detecting the presence of NOVX
CC in samples. Disorders that may be prevented, diagnosed and/or treated
CC vary depending on the NOVX protein. NOV1, NOV3, NOV5, NOV7, NOV9-11 and
CC NOV13-16 have casein kinase II phosphorylation sites characteristic of
CC serine/threonine kinases, and are used to treat kinase-related disorders
CC (e.g. Peutz-Jeghers syndrome, cellular proliferation and contraception).
CC NOV2-3, NOV6 and NOV8 are homologous to the epidermal growth factor (EGF)
CC -like super family and are involved in, e.g. regulation of cell
CC development, apoptosis, cell adhesion, growth migration, cell structure
CC and motility and protein management, and are used to treat cancers,
CC inflammatory disorders, immune disorders and cellular adhesion disorders.
CC NOV6-10 are homologous to EGF-like fibrillin proteins and are used to
CC treat cardiovascular disease e.g. hypertrophic cardiomyopathy, long-QT
CC syndrome and marfan syndrome
XX

SQ	Sequence	2483 BP; 619 A; 648 C; 639 G; 577 T; 0 U; 0 Other;
Query Match	54.6%; Score 1778.6; DB 4; Length 2483;	
Best Local Similarity	98.9%; Pred. No. 0;	
Matches 1790; Conservative	0; Mismatches 19; Indels 0; Gaps 0;	
Qy	122 AGCCTTTCATGAGGAGCTCGGTTAAAGATCGGACAAATACGGTTTAAATGCCCGGCT 181	
Db	569 ACCCTCTGATCTTCTGTACAGGTTAAAGATCGGACAAATACGGTTTAAATGCCCGGCT 628	
Qy	182 TCTTCGGTACCATGCTGCTGCCACAGCTCTTCTGAAAACCTGAAATGATCTC 241	
Db	629 TCTTCGGTACCATGCTGCTGCCACAGCTCTTCTGAAAACCTGAAATGATCTC 688	
Qy	242 AAATGCTACTTCCCTCCAAAGGAGCCAAATAGTCAATCTCCGTCCTCAGAGCACGGTGA 301	
Db	689 AAATGCTACTTCCCTCCAAAGGAGCCAAATAGTCAATCTCCGTCCTCAGAGCACGGTGA 748	
Qy	302 TATAAATTAAGGCTAAGATCATATCCAGTGATATCATCTAGTACTTAATGGGATTTGTTCA 361	
Db	749 TATAAACAATAAGGCTAAGATCATATCCAGTGATATCATCTAGTACTTAATGGGATTTGTTCA 808	
Qy	362 TATCATAGACAATTTGCTATCTCCAAAATTTGCTTATCACTCCCAAGACAACTCTGG 421	
Db	809 TATCATAGACAATTTGCTATCTCCAAAATTTGCTTATCACTCCCAAGACAACTCTGG 868	
Qy	422 AAGAATTTGCAAAATCTTACGACTTTGGCAACAACAATGGCTATCAATTAATTTAGCAA 481	
Db	869 AAGAATTTGCAAAATCTTACGACTTTGGCAACAACAATGGCTATCAATTAATTTAGCAA 928	
Qy	482 CTTAATACAGGACTCAGGTTTGTGAGTGTCTATCCAGATCCCATCCACACCCAGTCA 541	
Db	929 CTTAATACAGGACTCAGGTTTGTGAGTGTCTATCCAGATCCCATCCACACCCAGTCA 988	
Qy	542 TCTCTTCTCGCCACCGACCAAGCCCTCCATGCTTACCTGCTGTAACAACAGGACTTCCT 601	
Db	989 TCTCTTCTCGCCACCGACCAAGCCCTCCATGCTTACCTGCTGTAACAACAGGACTTCCT 1048	
Qy	602 GTTCAACCAAGACAACAAGGAGTGAAGGAGTATTTGAAGTTTCAATGTGTATGATAGCA 661	
Db	1049 GTTCAACCAAGACAACAAGGAGTGAAGGAGTATTTGAAGTTTCAATGTGTATGATAGCA 1108	
Qy	662 TGCACAGGTTTACGTTGTGATCTTCCACATCCATGCTGCTGGAAGACCTTCAAGGTT 721	
Db	1109 TGCACAGGTTTACGTTGTGATCTTCCACATCCATGCTGCTGGAAGACCTTCAAGGTT 1168	
Qy	722 AGAGCTGAGTGTGAATGTGGAGCTGGCAGGACATCGGTGACCTCTTTCTGAATGGCCA 781	
Db	1169 AGAGCTGAGTGTGAATGTGGAGCTGGCAGGACATCGGTGACCTCTTTCTGAATGGCCA 1228	
Qy	782 AACCTGCAGAAATTTGTCAGCGGAGCTCTTTGTTGACCTGGGTGTGGCCCTACGGCATTTGA 841	
Db	1229 AACCTGCAGAAATTTGTCAGCGGAGCTCTTTGTTGACCTGGGTGTGGCCCTACGGCATTTGA 1288	
Qy	842 CTGTCTGCTGATTCATCCACCTCGGGGCGCTGTGACACCTTTTACTACTTTTCGATGC 901	
Db	1289 CTGTCTGCTGATTCATCCACCTCGGGGCGCTGTGACACCTTTTACTACTTTTCGATGC 1348	
Qy	902 CTCGGGGAGTGTGGGAGCTGTGTCAATACTCCAGCTGCTGCAAGGGCTACTTTCCGGCGAGA 961	
Db	1349 CTCGGGGAGTGTGGGAGCTGTGTCAATACTCCAGCTGCTGCAAGGGCTACTTTCCGGCGAGA 1408	
Qy	962 GGGTGTGAAGCAGAAAGTGTCTCAACCTGCTCCCTCAAGAGGACCTTGAAGGCTGCG 1021	
Db	1409 GGGTGTGAAGCAGAAAGTGTCTCAACCTGCTCCCTCAAGAGGACCTTGAAGGCTGCG 1468	
Qy	1022 GGAGCGGTGACGCTGGTGATACAGATCCCGCAGGTGCTGCAAGGGCTACTTTCCGGCGAGA 1081	
Db	1469 GGAGCGGTGACGCTGGTGATACAGATCCCGCAGGTGCTGCAAGGGCTACTTTCCGGCGAGA 1528	
Qy	1082 CTGTGAGGCTTCCCTCGGAGGACAGATGCCCCGTTGAATTAACCGGGGTGTCTGCTTGA 1141	
Db	1529 CTGTGAGGCTTCCCTCGGAGGACAGATGCCCCGTTGAATTAACCGGGGTGTCTGCTTGA 1588	

Qy	1142 TCAGTACTCGGCCACCGAGAGTGTAAATGCAACACCGGCTTCAATGGGACGGCGTGTGA 1201	
Db	1589 TCAGTACTCGGCCACCGAGAGTGTAAATGCAACACCGGCTTCAATGGGACGGCGTGTGA 1648	
Qy	1202 GATGTGTGGCGGGGAGATTTCGGGCGCTGATTTGTCTGCCCTGTGGCTCTCAGACCAAG 1261	
Db	1649 GATGTGTGGCGGGGAGATTTCGGGCGCTGATTTGTCTGCCCTGTGGCTCTCAGACCAAG 1708	
Qy	1262 ACAGTGCATGATGCGATCAGCGGCTCGGGCAGTGCCTCTGTGAAAACGGGGTGGACAG 1321	
Db	1709 ACAGTGCATGATGCGATCAGCGGCTCGGGCAGTGCCTCTGTGAAAACGGGGTGGACAG 1768	
Qy	1322 CCCCTCTGTGTGACATCAGGAGCTTTTCCCTCTGAGTGTGACCCCTCTTGTCTTCTGCTCA 1381	
Db	1769 CCCCTCTGTGTGACATCAGGAGCTTTTGTCTGAGTGTGACCCCTCTTGTCTTCTGCTCA 1828	
Qy	1382 TGCCACCTGTAAAGGAGAAACAACGCTGTGAGTGTAAACCTGGATTAAGAGTGAACGGAAT 1441	
Db	1829 TGCCACCTGTAAAGGAGAAACAACGCTGTGAGTGTAAACCTGGATTAAGAGTGAACGGAAT 1888	
Qy	1442 CACATGCAAGTTTGTGGATTTCTGCAAAACAGGACAAACGGGGCTGTGAAAACGGTGGCCAG 1501	
Db	1889 CACATGCAAGTTTGTGGATTTCTGCAAAACAGGACAAACGGGGCTGTGAAAACGGTGGCCAG 1948	
Qy	1502 ATGCTCCCAGAAAGGCGACGAAGTCTCTGCAAGTGCACGAAGGGATACAAAGGGGACCG 1561	
Db	1949 ATGCTCCCAGAAAGGCGACGAAGTCTCTGCAAGTGCACGAAGGGATACAAAGGGGACCG 2008	
Qy	1562 GCACAGCTGCACAGAGATAGACCCCTGTGCAACAGCGCTTAAACGGAGGCTGTCAAGGACA 1621	
Db	2009 GCACAGCTGCACAGAGATAGACCCCTGTGCAACAGCGCTTAAACGGAGGCTGTCAAGGACA 2068	
Qy	1622 CGCCACCTGTAAAGTGCACAGCGCCGGGCAAGCACAGTGTGAGTGTAAAGTCACTATGT 1681	
Db	2069 CGCCACCTGTAAAGTGCACAGCGCCGGGCAAGCACAGTGTGAGTGTAAAGTCACTATGT 2128	
Qy	1682 CGGAGATGGGCTGAACTGTGAGCGGAGCAGTGTGCCCTTGAACCGCTGTACAGGACAA 1741	
Db	2129 CGGAGATGGGCTGAACTGTGAGCGGAGCAGTGTGCCCTTGAACCGCTGTACAGGACAA 2188	
Qy	1742 TGGGAGTGGCATGCGAGACCCCAATGTGTGCAACCTCCACTTCCAGGATACCACTGTGG 1801	
Db	2189 TGGGAGTGGCATGCGAGACCCCAATGTGTGCAACCTCCACTTCCAGGATACCACTGTGG 2248	
Qy	1802 GGTGTTCCATCTACGCTCCCACTGGGCCAGATTAAGCTGACCTTTGACAAAACGACAGA 1861	
Db	2249 GGTGTTCCATCTACGCTCCCACTGGGCCAGATTAAGCTGACCTTTGACAAAACGACAGA 2308	
Qy	1862 GGCTGTGCCAACGAAGCTGCGACCACTTGGCAACCTTCAACAGCTCTCTCTATGCCAGAA 1921	
Db	2309 GGCTGTGCCAACGAAGCTGCGACCACTTGGCAACCTTCAACAGCTCTCTCTATGCCAGAA 2368	
Qy	1922 GGCCAAGTA 1930	
Db	2369 GACCTGGTA 2377	

RESULT 11
AAP87117
ID AAP87117 standard; DNA; 2512 BP.
XX AC AC
XX XX
DT 26-MAR-2002 (first entry)
XX XX
DE NOV6 coding sequence.
XX NOV; Cytostatic; contraceptive; antiinflammatory; immunomodulatory;
KW cardiovascular; casein kinase II phosphorylation site; contraction;
KW serine/threonine kinase; Peutz-Jeghers syndrome; cellular proliferation;
KW epidermal growth factor; cell development; apoptosis; cell adhesion;
KW growth migration; cell structure; motility; cancer; immune disorder;

inflammatory disorder; cellular adhesion disorder; long-QT syndrome; cardiovascular disease; hypertrophic cardiomyopathy; marfan syndrome; therapy; NOV1; NOV2; NOV3; NOV4; NOV5; NOV6; NOV7; NOV8; NOV9; NOV10; NOV11; NOV12; NOV13; NOV14; NOV15; NOV16; ds.

Unidentified.

Key Location/Qualifiers
CDS 416..2425
/*tag= a
/product= "NOV6"

WO200136638-A2.

25-MAY-2001.

17-NOV-2000; 2000WO-US031543.

19-NOV-1999; 99US-0166336P.

29-NOV-1999; 99US-0167785P.

08-MAR-2000; 2000US-0187844P.

16-NOV-2000; 2000US-00715417.

(CURA-) CURAGEN CORP.

Shimkets RA, Lichenstein H, Vernet C, Fernandes E;

WPI; 2001-648134/74.

P-PSDB; AAB83362.

Novel human polypeptides and the nucleic acids that encode them useful for preventing, diagnosing and treating e.g. cancer, inflammation and immune disorders.

Claim 9; Page 24-25; 141pp; English.

This sequence encodes the NOV6 protein. The invention relates to the NOV1-NOV16 proteins, and their coding sequences. The proteins have Cytostatic ; contraceptive; antiinflammatory; immunomodulatory; and cardiovascular activities. The sequences may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate NOVX expression. They may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of protein by expressing inactive proteins or to supplement the patients own production of protein. They are used to produce NOVX proteins, by inserting the nucleic acid into a cell and culturing it to express the protein. The DNA may be used as DNA probes in assays to detect and quantitate the presence of similar DNAs in samples, and which patients may need restorative therapy. The NOVX protein may also be used as antigens in the production of antibodies (Abs) against NOVX and in assays to identify modulators of NOVX expression and activity. The anti-NOVX Abs and antagonist are used to down regulate expression and activity. The anti-NOVX Abs are used for detecting the presence of NOVX in samples. Disorders that may be prevented, diagnosed and/or treated vary depending on the NOVX protein. NOV1, NOV3, NOV5, NOV7, NOV9-11 and NOV13-16 have casein kinase II phosphorylation sites characteristic of serine/threonine kinases, and are used to treat kinase-related disorders (e.g. Peutz-Jeghers syndrome, cellular proliferation and contraction disorders NOV2-3, NOV6 and NOV8 are homologous to the epidermal growth factor (EGF) -like super family and are involved in, e.g. regulation of cell development, apoptosis, cell adhesion, growth migration, cell structure and motility and protein management, and are used to treat cancers, inflammatory disorders, immune disorders and cellular adhesion disorders. NOV6-10 are homologous to EGF-like fibrillin proteins and are used to treat cardiovascular disease e.g. hypertrophic cardiomyopathy, long-QT syndrome and marfan syndrome

Sequence 2512 BP; 623 A; 657 G; 581 T; 0 U; 0 Other;

Query Match 54.5%; Score 1777; DB 4; Length 2512;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 1789; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY	122	AGCCTTTGATGAGGAGCTCGGTTAAAGACTGGGACAAATACGGTTTAAATGCCAGGT	181
DB	598	ACCTCTGATCTCTCTTACAGGTTAAAGACTGGGACAAATACGGTTTAAATGCCAGGT	657
QY	182	TCTTCGGTACCAATGTGGTCCGCTGCCACCAAGCTGCTTCTGGAAAACCTGAAATTGATCTC	241
DB	658	TCTTCGGTACCAATGTGGTCCGCTGCCACCAAGCTGCTTCTGGAAAACCTGAAATTGATCTC	717
QY	242	AAATGCTACTCCCTCCAGGAGAGCCATAGTATCTCTCGTCTCTCAGAGCAGGTGTA	301
DB	718	AAATGCTACTCCCTCCAGGAGAGCCATAGTATCTCTCGTCTCTCAGAGCAGGTGTA	777
QY	302	TATAAATATATAGGCTAAGATCATATCCAGTGTATCATCAGTACTATTAATGGGATTGTTCA	361
DB	778	TATAAATATATAGGCTAAGATCATATCCAGTGTATCATCAGTACTATTAATGGGATTGTTCA	837
QY	362	TATCATAGACAAATTGCTATCTCCCAAAATTTGCTTATCATCTCCCAAGACAACTCTGG	421
DB	838	TATCATAGACAAATTGCTATCTCCCAAAATTTGCTTATCATCTCCCAAGACAACTCTGG	897
QY	422	AAGRAATCTGCAAAATCTTAGCACTTTGGCAACAAACATGCTACATCAATTTAGCAA	481
DB	898	AAGRAATCTGCAAAATCTTAGCACTTTGGCAACAAACATGCTACATCAATTTAGCAA	957
QY	482	CTTAATACAGGACTCAGGTTTGTGCTGAGTGTATCAACCGATCCATCCACACCCAGTCAAC	541
DB	958	CTTAATACAGGACTCAGGTTTGTGCTGAGTGTATCAACCGATCCATCCACACCCAGTCAAC	1017
QY	542	TCTCTTCTGGCCACCGACCAAGCCCTCAATGCCCTTACCTGCTGAACACAGGACTTCT	601
DB	1018	TCTCTTCTGGCCACCGACCAAGCCCTCAATGCCCTTACCTGCTGAACACAGGACTTCT	1077
QY	602	GTTCAACCAAGACAAACAGGACAGCTGGAAGAGTATTTGAAGTTTCAATGTGATACGAGA	661
DB	1078	GTTCAACCAAGACAAACAGGACAGCTGGAAGAGTATTTGAAGTTTCAATGTGATACGAGA	1137
QY	662	TGCCAAGGTTTTAGCTGTGGATCTTCCCAATCACTGCCTGGGAAGACCTTGAAGGTTTC	721
DB	1138	TGCCAAGGTTTTAGCTGTGGATCTTCCCAATCACTGCCTGGGAAGACCTTGAAGGTTTC	1197
QY	722	AGACTGAGTGTGAATGTGGAGCTGGCAGGACATCGGTGACCTCTTTTGAATGGCCA	781
DB	1198	AGACTGAGTGTGAATGTGGAGCTGGCAGGACATCGGTGACCTCTTTTGAATGGCCA	1257
QY	782	AACCTGCAGAAATCTGCAGCGGAGCTCTGTTGACCTGGGTGTGGCTACAGGATTTGA	841
DB	1258	AACCTGCAGAAATCTGCAGCGGAGCTCTGTTGACCTGGGTGTGGCTACAGGATTTGA	841
QY	842	CTGCTCTGATTTGATCCACCTCTGGGGGGCGCTGTGACACCTTTTACTCTTTTCGATGC	901
DB	1318	CTGCTCTGATTTGATCCACCTCTGGGGGGCGCTGTGACACCTTTTACTCTTTTCGATGC	1377
QY	902	CTCGGGGAGTGTGGGAGCTGTGTCAATATCCAGCTGCCCAAGGTGGAGTAAACAAA	961
DB	1378	CTCGGGGAGTGTGGGAGCTGTGTCAATATCCAGCTGCCCAAGGTGGAGTAAACAAA	1437
QY	962	GGGTGTCAAGCAGAAAGTCTCTACACCTGCCCTCAAGAGNACTTGAAGCTGCCG	1021
DB	1438	GGGTGTCAAGCAGAAAGTCTCTACACCTGCCCTCAAGAGNACTTGAAGCTGCCG	1497
QY	1022	GGAGCGGTGCAGGCTGTGTGATACAGATCCCGAGGTGCTCAAGGGCTTCTTCGGGGCAGA	1081
DB	1498	GGAGCGGTGCAGGCTGTGTGATACAGATCCCGAGGTGCTCAAGGGCTTCTTCGGGGCAGA	1557
QY	1082	CTGTCAAGCTGCCCTGGAGGACAGATGCCCGTGTAAATACCGGGGTCTCTGCCTTGA	1141
DB	1558	CTGTCAAGCTGCCCTGGAGGACAGATGCCCGTGTAAATACCGGGGTCTCTGCCTTGA	1617
QY	1142	TCAGTACTCGGCCACCGGAGGTGAATGCAACACGGCTTCAATGGGACGGCGTGTGA	1201
DB	1618	TCAGTACTCGGCCACCGGAGGTGAATGCAACACGGCTTCAATGGGACGGCGTGTGA	1677
QY	1202	GATGTGTGCGCGGGAGATTTCGGGCTGTGTTCTGCTGCCCTGTGCTCTCAGACACCGG	1261

Db 1301 CCTGTAGATGACAGCCCGGAGACAAAGTGTGAGTGTAAAGTCACTATGTCGGAG 1360
 QY 1687 ATGGGCTGAACCTGTAGCCGAGCAGCTGCCATTGACCGCTCTTACAGGACAAATGGGC 1746
 Db 1361 ATGGGCTGAACCTGTAGCCGAGCAGCTGCCATTGACCGCTCTTACAGGACAAATGGGC 1420
 QY 1747 AGTGCCATGACAGCCCAATGTGTGACCTCCACTTCAGGATACACTGTGTGGGGTGT 1806
 Db 1421 AGTGCCATGACAGCCCAATGTGTGACCTCCACTTCAGGATACACTGTGTGGGGTGT 1480
 QY 1807 TCCATCTAGCTCCCTGAGCCAGTATAGCTGACCTTTGACAAAGCCAGAGGCCT 1866
 Db 1481 TCCATCTAGCTCCCTGAGCCAGTATAGCTGACCTTTGACAAAGCCAGAGGCCT 1540
 QY 1867 GTGCCAAGAGCTGGACATGCGCACTTACCAACAGCTCTCTATGCCCCAGAG 1922
 Db 1541 GTGCCAAGAGCTGGACATGCGCACTTACCAACAGCTCTCTATGCCCCAGAG 1596

RESULT 14

AC76373
 ID AAC76373 standard; cDNA; 1377 BP.

XX AC AAC76373;

XX DT 08-FEB-2001 (first entry)

XX DE Human ORFX ORF1928 polynucleotide sequence SEQ ID NO:3855.

XX KW Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;
 KW vulnary; antiparkinsonian; nootropic; neuroprotective; osteopathic;
 KW anticonvulsant; thrombolytic; coagulant; vasotropic; antidiabetic;
 KW immunostimulant; dermatological; immunosuppressive; antiinflammatory;
 KW antianemic; gene therapy; cancer; proliferative disorder; hypertension;
 KW neurodegenerative disorder; osteoarthritis; graft vs host disease;
 KW cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
 KW cholesterol ester storage; systemic lupus erythematosus; infection;
 KW severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
 KW allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
 KW bone damage; cartilage damage; antiinflammatory disease; coagulation;
 KW thrombosis; contraceptive; ss.

XX OS Homo sapiens.

XX PN WO200058473-A2.

XX PD 05-OCT-2000.

XX PF 31-MAR-2000; 2000WO-US008621.

XX PR 31-MAR-1999; 99US-0127607P.

XX PR 02-APR-1999; 99US-0127636P.

XX PR 05-APR-1999; 99US-0127728P.

XX PR 30-MAR-2000; 2000US-00540763.

XX PA (CURA-) CURAGEN CORP.

XX XX Shimkets RA, Leach M;

XX PT WPI; 2000-602362/57.

XX DR P-PSDB; AAB42164.

XX PT Novel nucleic acids and peptides derived from open reading frame X,
 XX useful for treating e.g. cancers, proliferative disorders,
 XX neurodegenerative disorders and cardiovascular disease.

XX PS Claim 5; Page 3006-3007; 5507pp; English.

XX XX AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,
 CC which represent the human ORFX open reading frames 1 to 3161. The ORFX
 CC

CC sequences have activities such as: cytostatic; hepatotropic; vulnary;
 CC antiparkinsonian; nootropic; neuroprotective; osteopathic;
 CC anticonvulsant; antidiabetic; immunosuppressant; immunostimulant;
 CC cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive;
 CC dermatological; immunosuppressive; antiinflammatory; antibacterial;
 CC antiviral; antifungal; antirheumatic; antithyroid; and antianemic. The
 CC sequences can be used for determining the presence of or predisposition
 CC to, or preventing or treating pathological conditions associated with an
 CC ORFX-associated disorder. The nucleic acids can be used to express ORFX
 CC proteins in gene therapy vectors. The proteins and nucleic acids may be
 CC used to treat cancers, proliferative disorders, neurodegenerative
 CC disorders, osteoarthritis, graft vs host disease, cardiovascular disease,
 CC diabetes mellitus, hypertension, hypothyroidism, cholesterol ester
 CC storage, systemic lupus erythematosus, severe combined immunodeficiency
 CC (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune
 CC disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and
 CC cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to
 CC enhance coagulation; to inhibit thrombosis; and as a contraceptive
 XX

SQ Sequence 1377 BP; 303 A; 398 C; 342 G; 330 T; 0 U; 4 Other;

Query Match 41.3%; Score 1347.4; DB 3; Length 1377;

Best Local Similarity 99.6%; Pred. No. 0;

Matches 1371; Conservative 0; Mismatches 2; Indels 3; Gaps 2;

QY 1876 AAGCTGCGACCATGGCAACCTACAAACAGCTCTCTATGCCAGAGGCAAGTACCACC 1935
 Db 2 AAGCTGCGACCATGGCAACCTACAAACAGCTCTCTATGCCAGAGGCAAGTACCACC 61
 QY 1936 TGTGCTCAGCAGGCTGGTGGAGACCGGCGGGTTCCTTACCCACAGCTTCGCTCC 1995
 Db 62 TGTGCTCAGCAGGCTGGTGGAGACCGGCGGGTTCCTTACCCACAGCTTCGCTCC 121
 QY 1996 AGAAGCTGGCTCGCTGGTGGTGGATAGTGGACTATGGACCTAGACCCACAGAGTG 2055
 Db 122 AGAAGCTGGCTCGCTGGTGGTGGATAGTGGACTATGGACCTAGACCCACAGAGTG 181
 QY 2056 AAATGTGGAGTGTCTTCTGCTATCGGATGAAGATGTGAACCTGCACTGCAAGTGGGT 2115
 Db 182 AAATGTGGAGTGTCTTCTGCTATCGGATGAAGATGTGAACCTGCACTGCAAGTGGGT 241
 QY 2116 ATGTGGAGATGGCTTCTCATGCACTGGGAACTGTCTGAGTCTCTGATGTCTTCCCT 2175
 Db 242 ATGTGGAGATGGCTTCTCATGCACTGGGAACTGTCTGAGTCTCTGATGTCTTCCCT 301
 QY 2176 CACTCACAAACTTCTGACGGAAGTGTGGGCTATTCCAAAGCTCAGCTGAGGCGGTG 2235
 Db 302 CACTCACAAACTTCTGACGGAAGTGTGGGCTATTCCAAAGCTCAGCTGAGGCGGTG 361
 QY 2236 CATTTCTAGAACACTGACTGACCTGTCCATCCGCGGCACTCTTTGTGCCACAGACA 2295
 Db 362 CATTTCTAGAACACTGACTGACCTGTCCATCCGCGGCACTCTTTGTGCCACAGACA 421
 QY 2296 GTGGGCTGGGGAGAAATGAGACCTTGTCTGGGCGGACATCGAGCACCACTCGCCAATG 2355
 Db 422 GTGGGCTGGGGAGAAATGAGACCTTGTCTGGGCGGACATCGAGCACCACTCGCCAATG 481
 QY 2356 TCAGCATGTTTTTCTTCAATGACCTTGTCAATGGACCC-ACCCTGCAACAGAGGTGGGA 2414
 Db 482 TCAGCATGTTTTTCTTCAATGACCTTGTCAATGGACCCCTTCCAAACAGAGGTGGGA 541
 QY 2415 AGCAAGCTGTCTCATCATCTGCGCAGCAGGACCCACT--CCAAACCGAGGACCAAGTTTG 2472
 Db 542 AGCAAGCTGTCTCATCATCTGCGCAGCAGGACCCACTNNCCAAACCGAGGACCAAGTTTG 601
 QY 2473 TTGATGGAAGAGCAATTTCTGAGTGGACATCTTTTGCTTCCAATGGGATCATTCATGTCA 2532
 Db 602 TTGATGGAAGAGCAATTTCTGAGTGGACATCTTTTGCTTCCAATGGGATCATTCATGTCA 661
 QY 2533 TTTTCCAGGCTTTTAAAGCACCCTTCCCTCCCGGTGACCTTGACCACTGGGTGGAG 2592
 Db 662 TTTTCCAGGCTTTTAAAGCACCCTTCCCTCCCGGTGACCTTGACCACTGGGTGGAG 721

Db	481	CAGAAAGGCCAAGTACCACTGTGCTCAGCAGGCTGGCTGGAGACGGGCGGTTGCCTAC	540
QY	1977	CCACAGAGCTTCGGCTCCCAAGACGTGTGGCTCTGGTGTGGTGTGGATAGTGGAATATGGA	2036
Db	541	CCACAGAGCTTCGGCTCCCAAGACGTGTGGCTCTGGTGTGGTGTGGATAGTGGAATATGGA	600
QY	2037	CCTAGACCCAAACAGAGTGAATGTGGAGTGTCTTCTGCTATCCGATGAAGATGTGAAC	2096
Db	601	CCTAGACCCAAACAGAGTGAATGTGGAGTGTCTTCTGCTATCCGATGAAGATGTGAAC	660
QY	2097	TGCACCTGGAAGTGGGCTATGTGGAGATGGCTTCTCATGAGTGGGAACTGCTGCAG	2156
Db	661	TGCACCTGGAAGTGGGCTATGTGGAGATGGCTTCTCATGAGTGGGAACTGCTGCAG	720
QY	2157	GTCCCTGATGCTCTTCCCCTCACTACAAACCTTCTGTCGAGCGAAGTGTGGGCTATTCCAAC	2216
Db	721	GTCCCTGATGCTCTTCCCCTCACTACAAACCTTCTGTCGAGCGAAGTGTGGGCTATTCCAAC	780
QY	2217	AGCTCAGCTCGAGGCGGTGCATTTCTTAGAACCTCTGACTGACCTGTCCATCCGGGGCAAC	2276
Db	781	AGCTCAGCTCGAGGCGGTGCATTTCTTAGAACCTCTGACTGACCTGTCCATCCGGGGCAAC	840
QY	2277	CTCTTTGTGCCACAGAACAGTGGGCTGGGGAGAAATGAGACCTTGTCTGGGCGGGACATC	2336
Db	841	CTCTTTGTGCCACAGAACAGTGGGCTGGGGAGAAATGAGACCTTGTCTGGGCGGGACATC	900
QY	2337	GAGCACCACTTCGCAATGTCCAGCATGTTTTCTTACAATGACCTTGTCAATGGCACCAAC	2396
Db	901	GAGCACCACTTCGCAATGTCCAGCATGTTTTCTTACAATGACCTTGTCAATGGCACCAAC	960
QY	2397	CTGCACACGAGGTGGGAAGCAAGCTGCTCATCTACTGCCAGCAGGACCCACTCCCAACCG	2456
Db	961	CTGCACACGAGGTGGGAAGCAAGCTGCTCATCTACTGCCAGCAGGACCCACTCCCAACCG	1020
QY	2457	ACGGAGACCAAGTGTGTGATGGAGAGCCATCTTCGACGTGGGACATCTTTGGCCTCCAAAT	2516
Db	1021	ACGGAGACCAAGTGTGTGATGGAGAGACATCTTCGAGTGGGACATCTGTGCTCCCAAT	1080
QY	2517	GGGATCAATCATGTTCATTTCCAGGCTTTAAAAGCACCCCTGCCCGGTGACCTTGGAC	2576
Db	1081	GGGATCAACATGTTCATTTCCAGGCTTTAAAAGCACCCCTGCCCGGTGACCTTGGAC	1140
QY	2577	CACACTGGCTTGGAGCAGGATCTCTTTGCCATCATCTGTGTGACTGGGGCTGTGCC	2636
Db	1141	CACACTGGNTTGGAGNAGGATCTCTTGTGNCATCATCTGTGTGACTGGGGCTGTGCC	1200
QY	2637	TTGGCTCTTACTCTCTACTTTTCGGATAAACCGGAGAACATCGGCTTCCAGCATTTTGA	2695
Db	1201	TTGGCTCTTACTCTCTACTTTTCGGATAAACCGGAGAACATCGGCTTCCAGCATTTTGA	1259

Search completed: June 21, 2004, 10:47:18
Job time : 1193 secs

